



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 137481

TO: David Lukton
Location: REM-3B75/3C70
Art Unit: 1653
Tuesday, November 16, 2004

Case Serial Number: 09/943002

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Lukton,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524



SEARCH REQUEST FORM
(STIC)

Access DB# _____

Requestor's Name: David Lukton

Examiner number: 71263

Date: 11/9/04

Art Unit: 1653

Phone number: 571-272-0952

Serial Number:

09-943002

Mail Box: 3-C-70

Examiner Rm: 3-B-75

Results format: paper

Title: Novel reovirus-derived proteins and uses therefor

Applicant: Roy Duncan

Earliest Priority Date: 11/7/97

~~~~~

Please search SEQ ID NO: 14

RECEIVED  
NOV - 9 2004  
TECH/STIC

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2004, 14:47:10 ; Search time 40 Seconds  
(without alignments)  
232.113 Million cell updates/sec

Title: US-09-943-002-14

Perfect score: 720

Sequence: 1 MGRHSIVQPPAPPNAFVE.....EENTRLNHDRNPDGGINV 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5A COMB.pap.\*
- 2: /cgn2\_6/prodata/1/iaa/5B COMB.pap.\*
- 3: /cgn2\_6/prodata/1/iaa/6A COMB.pap.\*
- 4: /cgn2\_6/prodata/1/iaa/6B COMB.pap.\*
- 5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pap.\*
- 6: /cgn2\_6/prodata/1/iaa/backfilese1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description          |
|------------|-------|-------------|--------|----|----------------------|
| 1          | 85    | 11.8        | 159    | 4  | US-09-248-796A-16594 |
| 2          | 81    | 11.2        | 271    | 4  | US-09-252-991A-21522 |
| 3          | 80.5  | 11.2        | 415    | 4  | US-09-710-279-1406   |
| 4          | 80.5  | 11.2        | 458    | 3  | US-09-134-001C-4663  |
| 5          | 75.5  | 10.5        | 1220   | 2  | US-08-843-530B-36    |
| 6          | 75.5  | 10.5        | 1220   | 4  | US-09-636-728-32     |
| 7          | 74    | 10.3        | 408    | 2  | US-09-014-969-13     |
| 8          | 74    | 10.3        | 1726   | 4  | US-09-700-227-2      |
| 9          | 74    | 10.3        | 1739   | 4  | US-09-540-236-3739   |
| 10         | 73    | 10.1        | 482    | 4  | US-09-328-352-7794   |
| 11         | 72.5  | 10.1        | 338    | 4  | US-09-248-796A-26748 |
| 12         | 72.5  | 10.1        | 751    | 2  | US-08-843-530B-32    |
| 13         | 72.5  | 10.1        | 751    | 4  | US-09-636-728-29     |
| 14         | 71.5  | 9.9         | 1257   | 3  | US-08-611-729A-8     |
| 15         | 71.5  | 9.9         | 1257   | 4  | US-09-195-524-8      |
| 16         | 71    | 9.9         | 174    | 4  | US-09-134-000C-4758  |
| 17         | 70    | 9.7         | 507    | 4  | US-09-270-767-44005  |
| 18         | 69    | 9.6         | 306    | 4  | US-09-674-529B-2     |
| 19         | 69    | 9.6         | 315    | 4  | US-09-674-529B-6     |
| 20         | 68    | 9.4         | 1014   | 4  | US-10-101-464A-807   |
| 21         | 67    | 9.3         | 287    | 4  | US-09-543-681A-5282  |
| 22         | 67    | 9.3         | 306    | 4  | US-09-674-529B-4     |
| 23         | 67    | 9.3         | 309    | 4  | US-09-674-529B-12    |
| 24         | 67    | 9.3         | 315    | 4  | US-09-674-529B-8     |
| 25         | 67    | 9.3         | 393    | 4  | US-09-248-796A-18493 |
| 26         | 67    | 9.3         | 566    | 4  | US-09-543-681A-7802  |
| 27         | 66.5  | 9.2         | 215    | 4  | US-09-248-796A-23074 |

|    |      |     |     |   |                      |                   |
|----|------|-----|-----|---|----------------------|-------------------|
| 28 | 66.5 | 9.2 | 322 | 4 | US-09-543-681A-6839  | Sequence 6839, Ap |
| 29 | 66.5 | 9.2 | 516 | 4 | US-09-489-039A-12893 | Sequence 12893, A |
| 30 | 66.5 | 9.2 | 799 | 4 | US-09-165-396-4      | Sequence 4, Appli |
| 31 | 66   | 9.2 | 160 | 4 | US-09-270-767-59046  | Sequence 59046, A |
| 32 | 66   | 9.2 | 182 | 4 | US-09-540-236-2100   | Sequence 2100, Ap |
| 33 | 66   | 9.2 | 238 | 4 | US-09-710-279-3126   | Sequence 3126, Ap |
| 34 | 66   | 9.2 | 238 | 4 | US-09-710-279-3152   | Sequence 3152, Ap |
| 35 | 66   | 9.2 | 241 | 3 | US-09-134-001C-5598  | Sequence 5598, Ap |
| 36 | 66   | 9.2 | 355 | 4 | US-09-733-524A-12    | Sequence 12, Appl |
| 37 | 66   | 9.2 | 356 | 3 | US-09-092-315-12     | Sequence 12, Appl |
| 38 | 66   | 9.2 | 370 | 3 | US-09-142-551A-4     | Sequence 4, Appli |
| 39 | 66   | 9.2 | 393 | 4 | US-09-390-131-8      | Sequence 8, Appli |
| 40 | 66   | 9.2 | 396 | 3 | US-09-142-551A-3     | Sequence 3, Appli |
| 41 | 66   | 9.2 | 400 | 4 | US-09-538-092-1146   | Sequence 1146, Ap |
| 42 | 66   | 9.2 | 795 | 4 | US-09-270-767-43662  | Sequence 43662, A |
| 43 | 65.5 | 9.1 | 576 | 4 | US-09-134-000C-6480  | Sequence 6480, Ap |
| 44 | 65.5 | 9.1 | 579 | 4 | US-09-529-279-4      | Sequence 4, Appli |
| 45 | 65.5 | 9.1 | 579 | 4 | US-10-158-895-4      | Sequence 4, Appli |

ALIGNMENTS

RESULT 1  
US-09-248-796A-16594  
; Sequence 16594, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA  
; FILE REFERENCE: 107196.132  
; CURRENT FILING DATE: 1999-02-12  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 16594  
; LENGTH: 159  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-16594

|                                                                                     |       |                                                         |                                          |               |
|-------------------------------------------------------------------------------------|-------|---------------------------------------------------------|------------------------------------------|---------------|
| Query Match                                                                         | 11.8% | Score 85                                                | DB 4                                     | Length 159    |
| Best Local Similarity                                                               | 28.6% | Pred. NO. 0.071                                         |                                          |               |
| Matches                                                                             | 38    | Conservative                                            | 14                                       | Mismatches 61 |
|                                                                                     |       |                                                         | Indels                                   | 20            |
|                                                                                     |       |                                                         | Gaps                                     | 5             |
| QY                                                                                  | 18    | FVEIVSSSTGIIIAVGIFAFISFL---                             | YKLQWYNRKSQKQKQKQIRQIEQLGLLSYG           | 74            |
| Db                                                                                  | 17    | YVELSKRSTGGIAGIVIFIVIPISLISLGYNKKSKRNQKNTTPANITLGLSLNLE | 76                                       |               |
| QY                                                                                  | 75    | A-----GVASL-----                                        | PLLNVIHNPQSVISATPIYKGCCTGVNRLQLQITSGTAEN | 123           |
| Db                                                                                  | 77    | SQNVHQGVARIQQQQQQQQQQQQQLGTTSPEDHVPYPTQENDN--DLGRFDQGN  | 134                                      |               |
| QY                                                                                  | 124   | TRILNHDRNPDG                                            | 136                                      |               |
| Db                                                                                  | 135   | PHLN-----RPEG                                           | 143                                      |               |
| RESULT 2                                                                            |       |                                                         |                                          |               |
| US-09-252-991A-21522                                                                |       |                                                         |                                          |               |
| ; Sequence 21522, Application US/09252991A                                          |       |                                                         |                                          |               |
| ; Patent No. 6551795                                                                |       |                                                         |                                          |               |
| ; GENERAL INFORMATION:                                                              |       |                                                         |                                          |               |
| ; APPLICANT: Marc J. Rubenfield et al.                                              |       |                                                         |                                          |               |
| ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS |       |                                                         |                                          |               |
| ; FILE REFERENCE: 107196.136                                                        |       |                                                         |                                          |               |
| ; CURRENT FILING DATE: 1999-02-18                                                   |       |                                                         |                                          |               |

;; PRIOR APPLICATION NUMBER: US 60/074,788  
;; PRIOR FILING DATE: 1998-02-18  
;; PRIOR APPLICATION NUMBER: US 60/094,190  
;; PRIOR FILING DATE: 1998-07-27  
;; NUMBER OF SEQ ID NOS: 33142  
;; SEQ ID NO 21522  
;; LENGTH: 271  
;; TYPE: PRT  
;; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-21522

Query Match 11.2%; Score 81; DB 4; Length 271;  
Best Local Similarity 26.2%; Pred. No. 0.44;  
Matches 32; Conservative 25; Mismatches 53; Indels 12; Gaps 4;  
QY 13 PPNAFVEIVSSSTGIIIVGIFAFIFSLYKLOWNRKSNKKRKEQIREQIELGLLS 72  
DB 23 PPPRFPORLHSTGTMTSNDVDAEIAKFEALAHRWDRSEBPKPLHD--INFLRVNWD 80  
QY 73 YGAVASLPLLVIAHNPGSVISATPIYKGP-CTGVPN-----GRLLQITSGTAE 124  
DB 81 ERAGLAGKVDIGC--GGGILSEMAQRCANVTGIDMGEPALAVARLHQLSGVAVDYR 138  
QY 125 RI 126  
DB 139 QI 140

RESULT 3  
US-09-710-279-1406  
;; Sequence 1406, Application US/09710279  
;; Patent No. 6703492  
;; GENERAL INFORMATION:  
;; APPLICANT: KIMMERLY, WILLIAM JOHN  
;; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
;; FILE REFERENCE: PU3480US  
;; CURRENT APPLICATION NUMBER: US/09/710,279  
;; CURRENT FILING DATE: 2000-11-09  
;; PRIOR APPLICATION NUMBER: 60/164,258  
;; PRIOR FILING DATE: 1999-11-09  
;; NUMBER OF SEQ ID NOS: 4472  
;; SOFTWARE: Patentin Ver. 2.1  
;; SEQ ID NO 1406  
;; LENGTH: 415  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURES:  
;; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
;; OTHER INFORMATION: amino acid sequence  
;; FEATURE:  
;; NAME/KEY: MOD RES  
;; LOCATION: (415)  
;; OTHER INFORMATION: variable amino acid  
US-09-710-279-1406

Query Match 11.2%; Score 80.5; DB 4; Length 415;  
Best Local Similarity 34.0%; Pred. No. 0.91; Length 415;  
Matches 17; Conservative 13; Mismatches 19; Indels 1; Gaps 1;  
QY 33 GIFAFIFSLYKLOWNRKSNKKRKEQIREQIELGLLSYGAGV-ASLP 81  
DB 159 GVHAEPTTFGVKALWYTEMKRNLFKEVKEIEVGMKSGAVGTTFANIP 208

RESULT 4  
US-09-134-001C-4663  
;; Sequence 4663, Application US/09134001C  
;; Patent No. 6380370  
;; GENERAL INFORMATION:  
;; APPLICANT: Lynn Doucette-Stamm et al  
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
;; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
;; FILE REFERENCE: GTC-007

;; CURRENT APPLICATION NUMBER: US/09/134,001C  
;; CURRENT FILING DATE: 1998-08-13  
;; PRIOR APPLICATION NUMBER: US 60/064,964  
;; PRIOR FILING DATE: 1997-11-08  
;; PRIOR APPLICATION NUMBER: US 60/055,779  
;; PRIOR FILING DATE: 1997-08-14  
;; NUMBER OF SEQ ID NOS: 5674  
;; SEQ ID NO 4663  
;; LENGTH: 458  
;; TYPE: PRT  
;; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4663

Query Match 11.2%; Score 80.5; DB 3; Length 458;  
Best Local Similarity 34.0%; Pred. No. 1.1;  
Matches 17; Conservative 13; Mismatches 19; Indels 1; Gaps 1;  
QY 33 GIFAFIFSLYKLOWNRKSNKKRKEQIREQIELGLLSYGAGV-ASLP 81  
DB 169 GVHAEPTTFGVKALWYTEMKRNLFKEVKEIEVGMKSGAVGTTFANIP 218

RESULT 5  
US-08-843-530B-36  
;; Sequence 36, Application US/08843530B  
;; Patent No. 5939306  
;; GENERAL INFORMATION:  
;; APPLICANT: Selitrennikoff, Claude  
;; APPLICANT: Agnan, Jacqueline  
;; APPLICANT: Alex, Lisa A.  
;; APPLICANT: Simon, Melvin I.  
;; TITLE OF INVENTION: Osmosensing Histidine Kinases  
;; NUMBER OF SEQUENCES: 36  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSES: Medien & Carroll, LLP  
;; STREET: 220 Montgomery Street, Suite 2200  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: United States of America  
;; ZIP: 94104  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/843,530B  
;; FILING DATE: 16-APR-1997  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MacKnight, Kamrin T.  
;; REGISTRATION NUMBER: 38,230  
;; REFERENCE/DOCKET NUMBER: UTC-02717  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 705-8410  
;; TELEFAX: (415) 397-8338  
;; INFORMATION FOR SEQ ID NO: 36:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1220 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: not relevant  
;; TOPOLOGY: not relevant  
;; MOLECULE TYPE: protein  
US-08-843-530B-36

Query Match 10.5%; Score 75.5; DB 2; Length 1220;  
Best Local Similarity 23.3%; Pred. No. 16;  
Matches 31; Conservative 22; Mismatches 53; Indels 27; Gaps 6;  
QY 1 MCQRHSIVQPPAPPNFAFVEIVSSSTGIIIVGIFAFIFSLYKLOWNRKSNKKRKE 60  
DB 317 VSQPSVFLSPA-----TKLAKITGVTAIGVFLITL--PLAHW-----AVQP 360



```
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26748
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-26748

Query Match 10.1%; Score 72.5; DB 4; Length 338;
Best Local Similarity 22.8%; Pred. No. 5.8;
Matches 26; Conservative 17; Mismatches 42; Indels 29; Gaps 3;

QY 34 IFAPFISFLYKLLQWYNRKSKNKKKEQ-----IREQ-----IELGLLSYGAG 76
Db 158 IFALYGCVLFEWATWIANKEYDENKEETNLAIRKREWAISLAWYLAPSAALFLAYGAA 217
QY 77 VASLPLLVIANPQSVI-----SATPIYKGPCTGVPNSRLLOITSG 118
Db 218 LFPTKLVRIIWLPGFVEHIKFTSPFIPGRPTPVYVPLENLKRKHTSRVWTG 271

RESULT 12
US-08-843-5308-32
; Sequence 32, Application US/088435308
; Patent No. 5939306
; GENERAL INFORMATION:
; APPLICANT: Selitrennikoff, Claude
; APPLICANT: Agnan, Jacqueline
; APPLICANT: Alex, Lisa A.
; TITLE OF INVENTION: Osmosensing Histidine Kinases
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESS: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/843,5308
; FILING DATE: 16-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: UTC-02717
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein

; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3739
; LENGTH: 1739
; TYPE: PRT
; ORGANISM: M. catarrhalis
; US-09-540-236-3739

Query Match 10.3%; Score 74; DB 4; Length 1739;
Best Local Similarity 23.5%; Pred. No. 39;
Matches 36; Conservative 24; Mismatches 43; Indels 50; Gaps 8;

QY 17 AFVEIVSSSTGIIIVGIPAFISPL-----YKLLQWYN-RKSKN--KKRKE 60
Db 1494 SPFVVGDIQGFVEAQTVDGHDVFATIGLPLGSDVAQKAHAKKAYDTAKSANDVGMKS 1553
QY 61 QIREQIELGLLSYGAGVASLPLLVIANPQSVISATPIYKGPCTGVPNSRLLOITSG-- 118
Db 1554 ALQEGVD-----VLKQNGK--AGTPVVSQPVSGVQAGR--QIRSGQA 1592
QY 119 -----TAENRTRILNHGR-----NPDGGINV 140
Db 1593 NIAGYTIDKNGRLHNRGQTPDPNPRVSTNL 1625

RESULT 10
US-09-328-352-7784
; Sequence 7784, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7784
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-7784

Query Match 10.1%; Score 73; DB 4; Length 482;
Best Local Similarity 30.6%; Pred. No. 8.4;
Matches 34; Conservative 13; Mismatches 38; Indels 26; Gaps 6;

QY 15 PNAF-----VEIVSSSTGIIIVGIPAFISFLYKLLQWYNRKSKNKKKEQIR 63
Db 276 PNGFDPAVGLADYTDV--AKTGAWVGL-ALIVGIISAILFDYQVVVN--FREGIN 330
QY 64 EQIELGLLS-----XCAGVASLPLLVIANPQSVISATPIYKGPCT 105
Db 331 ASIGSLLAVMTASEYGVGAIIASIPGAMISHAMSSITFT-NPLVNGAVT 380

RESULT 11
US-09-248-796A-26748
; Sequence 26748, Application US/09248796A
```

```
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26748
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-26748

Query Match 10.1%; Score 72.5; DB 4; Length 338;
Best Local Similarity 22.8%; Pred. No. 5.8;
Matches 26; Conservative 17; Mismatches 42; Indels 29; Gaps 3;

QY 34 IFAPFISFLYKLLQWYNRKSKNKKKEQ-----IREQ-----IELGLLSYGAG 76
Db 158 IFALYGCVLFEWATWIANKEYDENKEETNLAIRKREWAISLAWYLAPSAALFLAYGAA 217
QY 77 VASLPLLVIANPQSVI-----SATPIYKGPCTGVPNSRLLOITSG 118
Db 218 LFPTKLVRIIWLPGFVEHIKFTSPFIPGRPTPVYVPLENLKRKHTSRVWTG 271

RESULT 12
US-08-843-5308-32
; Sequence 32, Application US/088435308
; Patent No. 5939306
; GENERAL INFORMATION:
; APPLICANT: Selitrennikoff, Claude
; APPLICANT: Agnan, Jacqueline
; APPLICANT: Alex, Lisa A.
; TITLE OF INVENTION: Osmosensing Histidine Kinases
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESS: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/843,5308
; FILING DATE: 16-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: UTC-02717
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
```

US-08-843-530B-32

Query Match 10.1%; Score 72.5; DB 2; Length 751;  
Best Local Similarity 24.0%; Pred. No. 18;  
Matches 31; Conservative 22; Mismatches 43; Indels 33; Gaps 7;  
QY 15 PNAFVEISSGIIIAVGIFAPISFLYKLLQWNRKSKKKRKEIQEIQELGLLSYG 74  
DB 280 PESLAKII---TGTVIAIGVFVILLTL--PLAHW-----AVQPIVRLQKATELITEG 326  
QY 75 AGVASLPLLNVAHNPFGSVISATPIYKPGCTG--VPNSRLLOITSGTAENTRIHLNHDGR 132  
DB 327 RGLS-----RASSPKRGPSGFAVPSS--LLQFNFAEAGSTTSVSGHGS 369  
QY 133 -NPDGSINV 140  
DB 370 GHGGAANY 378

## RESULT 13

US-09-636-728-29  
; Sequence 29, Application US/09636728  
; Patent No. 6716625  
; GENERAL INFORMATION:  
; APPLICANT: Selitrennikoff, Claude  
; APPLICANT: Pott, Greg  
; TITLE OF INVENTION: Histidine Kinases of Aspergillus and Other Fungal  
; FILE REFERENCE: UTC-03758  
; CURRENT APPLICATION NUMBER: US/09/636,728  
; PRIOR FILING DATE: 2000-08-09  
; PRIOR APPLICATION NUMBER: 08/843,530  
; FILING DATE: 1997-04-16  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 29  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-09-636-728-29

Query Match 10.1%; Score 72.5; DB 4; Length 751;  
Best Local Similarity 24.0%; Pred. No. 18;  
Matches 31; Conservative 22; Mismatches 43; Indels 33; Gaps 7;  
QY 15 PNAFVEISSGIIIAVGIFAPISFLYKLLQWNRKSKKKRKEIQEIQELGLLSYG 74  
DB 280 PESLAKII---TGTVIAIGVFVILLTL--PLAHW-----AVQPIVRLQKATELITEG 326  
QY 75 AGVASLPLLNVAHNPFGSVISATPIYKPGCTG--VPNSRLLOITSGTAENTRIHLNHDGR 132  
DB 327 RGLS-----RASSPKRGPSGFAVPSS--LLQFNFAEAGSTTSVSGHGS 369  
QY 133 -NPDGSINV 140  
DB 370 GHGGAANY 378

## RESULT 14

US-08-611-729A-8  
; Sequence 8, Application US/08611729A  
; Patent No. 6004924  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; APPLICANT: Henrique, Domingos M.P.  
; APPLICANT: Lewis, Julian H.  
; APPLICANT: Myat, Anna M.  
; APPLICANT: Fleming, Robert J.  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Mann, Robert S.  
; APPLICANT: Gray, Grace E.  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE

NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/611,729A  
FILING DATE: 06-MAR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7326-037  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1257 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-611-729A-8

Query Match 9.9%; Score 71.5; DB 3; Length 1257;

Best Local Similarity 27.3%; Pred. No. 49;  
Matches 42; Conservative 18; Mismatches 63; Indels 31; Gaps 8;

QY 2 QORHSIVQPPPPNAP-----VEIV---SSSTGIIIAV--GIFAFIPSLYKLLQ 47  
DB 874 GAHAIVAATQGNSSLLLATVETVVTGGSTGLLVPLCGAFSVMLACVVLVCV 933  
QY 48 WYNRSKNNKKEIQEIQELGLLSYGAGVASLPLLNVAHNP 100  
DB 934 WMT-----KRRKERERSLPREESANNOWAPLNPI-ERPGRHVDVLYQCKNFTPPP 988  
QY 101 KPCTGVNSRLLOITSGTAENTRIHLNHDGRNP 134  
DB 989 RRRCPGRPATR---PSGRM-RRTRILAAVRTP 1017

## RESULT 15

US-09-193-524-8  
; Sequence 8, Application US/09195524  
; Patent No. 6703489  
; GENERAL INFORMATION:  
; APPLICANT: Ish-Horowicz, David  
; APPLICANT: Henrique, Domingos M.P.  
; APPLICANT: Lewis, Julian H.  
; APPLICANT: Myat, Anna M.  
; APPLICANT: Fleming, Robert J.  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Mann, Robert S.  
; APPLICANT: Gray, Grace E.  
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE  
; TITLE OF INVENTION: SERRATE GENE AND METHODS BASED THEREON  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/09/195,524  
APPLICATION NUMBER: US/09/195,524  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/611,729  
FILING DATE: 06-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 7326-037  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1257 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-09-195-524-8

Query Match 9.9%; Score 71.5; DB 4; Length 1257;  
Best Local Similarity 27.3%; Pred. No. 49;  
Matches 42; Conservative 18; Mismatches 63; Indels 31; Gaps 8;  
QY 2 GQRHSIVOPPPAPPNAP-----VEIV---SSSTGIIIAV--GIFAFIFGFLYKLLQ 47  
DB 874 GAHAIVAATQGNSSLLLAIVTEVKVETVTGSSSTGLLVPLCGAFSVLWLCVVLV 933  
QY 48 WYNRKSKNKKRQIREQIBGLLSYGAGVASLPLNLNVIHNP-----SVISATPIY 100  
DB 934 WTR-----KKRKERSRLPREESANNQWAPLNPINPI-ERPGHKDVLVYQCKNFTPPP 988  
QY 101 KGECTGVPSNELLQITSGTAENTRIINHGRNP 134  
DB 989 RRCPCGRPATR-----PSGRM-RRTRILAAVRTP 1017

Search completed: November 15, 2004, 14:59:04  
Job time : 42 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:31:00 ; Search time 155 Seconds  
(without alignments)  
324.014 Million cell updates/sec

Title: US-09-943-002-14  
Perfect score: 720  
Sequence: 1 MGQRHSIVQPPAPPNAFV.....EENTRLNHDGRNPDGINSV 140

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 720   | 100.0       | 140    | 2     | AY06113 Baboon re  |
| 2          | 84    | 11.7        | 431    | 4     | AU33910 Staphyloc  |
| 3          | 84    | 11.7        | 431    | 4     | AU33695 Staphyloc  |
| 4          | 84    | 11.7        | 431    | 6     | ABU16411 Protein e |
| 5          | 84    | 11.7        | 454    | 6     | ABM71462 Staphyloc |
| 6          | 84    | 11.7        | 454    | 8     | ADO25483 S aureus  |
| 7          | 81    | 11.2        | 271    | 7     | ABO72776 Pseudomon |
| 8          | 80.5  | 11.2        | 415    | 4     | AG82156 S. epider  |
| 9          | 80.5  | 11.2        | 431    | 6     | ABU43432 Protein e |
| 10         | 80.5  | 11.2        | 431    | 6     | ABU42716 Protein e |
| 11         | 80.5  | 11.2        | 458    | 5     | ABP39818 Staphyloc |
| 12         | 79    | 11.0        | 454    | 8     | ADO25485 S aureus  |
| 13         | 78    | 10.8        | 391    | 5     | ABB48477 Listeria  |
| 14         | 78    | 10.8        | 391    | 6     | ABU32700 Protein e |
| 15         | 77.5  | 10.8        | 339    | 6     | ABU26499 Protein e |
| 16         | 77    | 10.7        | 852    | 4     | ABG13686 Novel hum |
| 17         | 76.5  | 10.6        | 681    | 5     | ABB93650 Herbicida |
| 18         | 75.5  | 10.5        | 427    | 7     | ADK61938 Disease t |
| 19         | 75.5  | 10.5        | 1220   | 8     | ADN07100 S. cerevi |
| 20         | 75    | 10.4        | 892    | 7     | ADJ68848 Human hea |
| 21         | 74.5  | 10.3        | 231    | 6     | ABR41590 Human DIT |
| 22         | 74.5  | 10.3        | 319    | 6     | ABM72920 Staphyloc |
| 23         | 74.5  | 10.3        | 498    | 4     | AAg92924 C glutami |
| 24         | 74    | 10.3        | 408    | 2     | AAW75856 Human sec |
| 25         | 74    | 10.3        | 408    | 2     | AY45161 Human sec  |

|    |      |      |      |   |                    |
|----|------|------|------|---|--------------------|
| 26 | 74   | 10.3 | 1455 | 4 | AAM80143 Human pro |
| 27 | 74   | 10.3 | 1726 | 3 | AY57572 Moraxella  |
| 28 | 74   | 10.3 | 1739 | 8 | ADL06053 M. catarr |
| 29 | 73.5 | 10.2 | 348  | 6 | ADA48468 Rice prot |
| 30 | 73.5 | 10.2 | 494  | 4 | ABB61632 Drosophil |
| 31 | 73.5 | 10.2 | 534  | 2 | AAZ26967 Wheat Mlo |
| 32 | 73.5 | 10.2 | 534  | 3 | AA801805 Wheat Mlo |
| 33 | 73.5 | 10.2 | 534  | 4 | AA831251 Amino aci |
| 34 | 73   | 10.1 | 262  | 6 | ABU31472 Protein e |
| 35 | 73   | 10.1 | 482  | 6 | ADA36497 Acinetoba |
| 36 | 73   | 10.1 | 543  | 8 | ADH71860 Human pro |
| 37 | 73   | 10.1 | 766  | 5 | ABG96273 Human imm |
| 38 | 73   | 10.1 | 766  | 8 | ADH71856 Human pro |
| 39 | 72.5 | 10.1 | 534  | 2 | AAZ26968 Wheat Mlo |
| 40 | 72.5 | 10.1 | 534  | 4 | AA831252 Amino aci |
| 41 | 72.5 | 10.1 | 751  | 8 | ADN07097 S. cerevi |
| 42 | 72.5 | 10.1 | 1677 | 8 | ADP76092 Arabidops |
| 43 | 72   | 10.0 | 649  | 8 | ADM48283 Polypepti |
| 44 | 72   | 10.0 | 687  | 7 | ADB64828 Human pro |
| 45 | 72   | 10.0 | 775  | 4 | AA893302 Human pro |

ALIGNMENTS

RESULT 1  
AY06113  
ID AY06113 standard; protein; 140 AA.  
XX AC AY06113;  
XX DT 16-AUG-1999 (first entry)  
XX DE Baboon reovirus fusogenic protein P15a.  
XX KW Orthoreovirus; reovirus; BRV; P15 protein; fusogenic protein;  
XX KW cell fusion; membrane fusion; syncytium formation.  
XX OS Baboon reovirus.  
XX FH Key Location/Qualifiers  
XX FT Domain 27..41  
XX FT /note= "transmembrane domain"  
XX PN WO9924582-A1.  
XX PD 20-MAY-1999.  
XX PF 06-NOV-1998; 98WO-CA001046.  
XX PR 07-NOV-1997; 97US-00965708.  
XX FA (UYDA-) UNIV DALHOUSIE.  
XX PI Duncan R;  
XX DR WPI; 1999-327410/27.  
XX DR N-PSDB; AAX58670.  
XX PT Fusogenic proteins from non-enveloped reoviruses.  
XX PS Example 6; Page 53-54; 57pp; English.  
XX CC The present sequence represents the fusogenic protein P15a of baboon reovirus (BRV). 2 Unrelated fusion proteins responsible for cell-cell fusion induced by avian reovirus (ARV) and the only 2 fusogenic mammalian reoviruses, Nelson Bay virus (NBV) and BRV, are identified in this invention. These proteins are termed P11 for ARV and NBV (see also AY06104, AY06107 and AY06110) and P15 for BRV. Fusogenic P11 and P15 are useful for (i) promoting fusion of cell, liposome or proteoliposome membranes; production of B and T cell hybridomas or other heterokaryons (they eliminate the need to use toxic chemicals such as PEG); (iii) for producing fusions between liposomes and cells or other liposomes; and

CC (iv) for incorporation into liposomes to allow intra- or extracellular  
 CC delivery of bioactive agents (e.g. nucleic acid, proteins and metabolic  
 CC regulators), both in vivo and in cell cultures. Antibodies raised against  
 CC p11 or p15 are useful for diagnosis and therapeutically (e.g. to block  
 CC undesirable fusion processes). P11 and P15 are smaller than fusogenic  
 CC proteins from enveloped viruses and are not glycosylated, so are easier  
 CC to produce and purify using recombinant expression systems. They do not  
 CC require a signal peptide for membrane entry, are not immunogenic and are  
 CC functional at neutral pH

XX Sequence 140 AA;

4 Query Match 100.0%; Score 720; DB 2; Length 140;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-72;  
 Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCQRHSIVQPPAPPNAFVEIVSSSTGIIIVGIFAFIFSLYKLLQWYNRKSNNKXKE 60

DB 1 MCQRHSIVQPPAPPNAFVEIVSSSTGIIIVGIFAFIFSLYKLLQWYNRKSNNKXKE 60

QY 61 QIREQIELGLLYGAGVASLPLNLVIAHNPVSVISATPIYKGPCTGVPSNRLLOITSGTA 120

DB 61 QIREQIELGLLYGAGVASLPLNLVIAHNPVSVISATPIYKGPCTGVPSNRLLOITSGTA 120

QY 121 ENTRILNHDGRNPDGSINV 140

DB 121 ENTRILNHDGRNPDGSINV 140

#### RESULT 2

AAU33910  
 ID AAU33910 standard; protein; 431 AA.

XX AAU33910;

DT 14-FEB-2002 (first entry)

XX Staphylococcus aureus cellular proliferation protein #186.

DE Antisense; prokaryotic cellular proliferation protein; antibiotic;  
 KW antibacterial; drug design.

XX Staphylococcus aureus.

OS WO200170955-A2.

PN 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009180.

XX 21-MAR-2000; 2000US-0191078P.

PR 23-MAY-2000; 2000US-0206848P.

PR 26-MAY-2000; 2000US-0207727P.

PR 23-OCT-2000; 2000US-0242578P.

PR 27-NOV-2000; 2000US-0253625P.

PR 22-DEC-2000; 2000US-0257931P.

PR 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;

PI Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

DR N-PSDB; AAS51769.

XX New polynucleotides for the identification and development of  
 PT antibiotics, comprise sequences of antisense nucleic acids.

XX Example 3; SEQ ID NO 5406; 51pp; English.

XX The invention relates to antisense inhibitors of genes essential to  
 CC prokaryotic cellular proliferation, their use in identifying the genes,

CC their use in the discovery of novel antibiotics, the essential genes  
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia  
 CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
 CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also  
 CC useful for the identification of potential new targets for antibiotic  
 CC development. The antisense nucleic acids can also be used to identify  
 CC proteins used in proliferation, to express these proteins, and to obtain  
 CC antibodies capable of binding to the expressed proteins. The proteins can  
 CC be used to screen compounds in rational drug discovery programmes. The  
 CC antisense nucleic acid sequence is also useful to screen for homologous  
 CC nucleic acids which are required for cell proliferation in a wide variety  
 CC of organisms. The present sequence represents an essential prokaryotic  
 CC cellular proliferation protein. Note: The sequence data for this patent  
 CC did not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 431 AA;

Query Match 11.7%; Score 84; DB 4; Length 431;  
 Best Local Similarity 26.5%; Pred. No. 2.2;  
 Matches 26; Conservative 15; Mismatches 35; Indels 22; Gaps 2;

QY 33 GIFAPIFSLYKLLQWYNRKSNNKXKEQIREQIELGLLYGAGVASLPLNLVIAHNPQS 92

DB 142 GVHAEPTTFGVKMLWYTEMQRNLQRPQVRBEIEVGKMSGAVG-----TFANIPPE 193

QY 93 VISATPIYKGPCTGVPSNRLLOITSGTAENTRIILNHD 130

DB 194 IESYVCKHLG-----IGTAPVSTQTLQRD 217

#### RESULT 3

AAU36895  
 ID AAU36895 standard; protein; 431 AA.

XX AAU36895;

DT 14-FEB-2002 (first entry)

XX Staphylococcus aureus cellular proliferation protein #1055.

DE Antisense; prokaryotic cellular proliferation protein; antibiotic;  
 KW antibacterial; drug design.

XX Staphylococcus aureus.

OS WO200170955-A2.

PN 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009180.

PR 21-MAR-2000; 2000US-0191078P.

PR 23-MAY-2000; 2000US-0206848P.

PR 26-MAY-2000; 2000US-0207727P.

PR 23-OCT-2000; 2000US-0242578P.

PR 27-NOV-2000; 2000US-0253625P.

PR 22-DEC-2000; 2000US-0257931P.

PR 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;

PI Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

DR N-PSDB; AAS54754.

XX New polynucleotides for the identification and development of  
 PT antibiotics, comprise sequences of antisense nucleic acids.

XX Example 3; SEQ ID NO 12488; 51pp; English.

XX The invention relates to antisense inhibitors of genes essential to  
 CC prokaryotic cellular proliferation, their use in identifying the genes,  
 CC themselves and the discovery of novel antibiotics, the essential genes  
 CC colli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
 CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also  
 CC useful for the identification of potential new targets for antibiotic  
 CC development. The antisense nucleic acids can also be used to identify  
 CC proteins used in proliferation, to express these proteins, and to obtain  
 CC antibodies capable of binding to the expressed proteins. The proteins can  
 CC be used to screen compounds in rational drug discovery programmes. The  
 CC antisense nucleic acid sequence is also useful to screen for homologous  
 CC nucleic acids which are required for cell proliferation in a wide variety  
 CC of organisms. The present sequence represents an essential prokaryotic  
 CC cellular proliferation protein. Note: The sequence data for this patent  
 CC did not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 431 AA;

Query Match 11.7%; Score 84; DB 4; Length 431;  
 Best Local Similarity 26.5%; Pred. No. 2.2;  
 : Matches 26; Conservative 15; Mismatches 35; Indels 22; Gaps 2;  
 QY 33 GIPAFIFLYKLLWYNRKSKKKEQIREQIELGLLSYGAGVASLPLLNVAHNPGS 92  
 DB 142 GVHAEPTTGVKQWALWYTEMQRNLQRFKQVRBIEVGMKSGAVG-----TFANIPPE 193  
 QY 93 VISATPIYKPGCTGVPSNRLQLTQTSPTAENTRILNHD 130  
 DB 194 IESVCKHLG-----IGTAPVSTQTLQRD 217

RESULT 4  
 ABU16411 standard; protein; 431 AA.  
 XX ABU16411;  
 AC ABU16411;  
 XX 19-JUN-2003 (first entry)  
 XX Protein encoded by Prokaryotic essential gene #1938.  
 XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 XX Staphylococcus aureus.  
 XX WO200277183-A2.  
 XX 03-OCT-2002.  
 XX 21-MAR-2002; 2002WO-US009107.  
 XX 21-MAR-2001; 2001US-00815242.  
 XX 06-SEP-2001; 2001US-00948993.  
 XX 25-OCT-2001; 2001US-0342923P.  
 XX 08-FEB-2002; 2002US-00072851.  
 XX 06-MAR-2002; 2002US-0362699P.  
 XX (ELIT-) ELITRA PHARM INC.  
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
 XX Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;  
 XX WPI; 2003-029926/02.  
 XX N-PSDB; ACA20281.  
 XX New antisense nucleic acids, useful for identifying proteins or screening  
 XX for homologous nucleic acids required for cellular proliferation to  
 XX isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 44335; 1766pp; English.

PS The invention relates to an isolated nucleic acid comprising any one of  
 XX the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 431 AA;

Query Match 11.7%; Score 84; DB 6; Length 431;  
 Best Local Similarity 26.5%; Pred. No. 2.2;  
 Matches 26; Conservative 15; Mismatches 35; Indels 22; Gaps 2;  
 QY 33 GIPAFIFLYKLLWYNRKSKKKEQIREQIELGLLSYGAGVASLPLLNVAHNPGS 92  
 DB 142 GVHAEPTTGVKQWALWYTEMQRNLQRFKQVRBIEVGMKSGAVG-----TFANIPPE 193  
 QY 93 VISATPIYKPGCTGVPSNRLQLTQTSPTAENTRILNHD 130  
 DB 194 IESVCKHLG-----IGTAPVSTQTLQRD 217

RESULT 5  
 ABM71462 standard; protein; 454 AA.  
 XX ABM71462;  
 XX 20-NOV-2003 (first entry)  
 XX Staphylococcus aureus protein #702.  
 XX Antisense; vaccine; gene therapy; infection; sepsis; diagnosis;  
 XX enzymatic assay; antibiotic target.  
 XX Staphylococcus aureus.  
 XX WO200294868-A2.  
 XX 28-NOV-2002.  
 XX 27-MAR-2002; 2002WO-IB002637.  
 XX 27-MAR-2001; 2001GB-00007661.  
 XX (CHIR-) CHIRON SPA.

PR 07-NOV-2002; 2002US-0424664P.  
PR 07-NOV-2002; 2002US-0424665P.  
PR 08-NOV-2002; 2002US-0424968P.  
PR 08-NOV-2002; 2002US-0425076P.  
PR 08-NOV-2002; 2002US-0425085P.  
PR 08-NOV-2002; 2002US-0425118P.  
PR 08-NOV-2002; 2002US-0425126P.  
PR 08-NOV-2002; 2002US-0425162P.  
PR 08-NOV-2002; 2002US-0425201P.  
PR 12-MAR-2003; 2003US-0453914P.  
PR 12-MAR-2003; 2003US-0454021P.  
PR 12-MAR-2003; 2003US-0454128P.  
PR 12-MAR-2003; 2003US-0454193P.  
PR 13-MAR-2003; 2003US-0454215P.  
PR 13-MAR-2003; 2003US-0454218P.  
PR 13-MAR-2003; 2003US-0454487P.  
PR 13-MAR-2003; 2003US-0454507P.  
PR 13-MAR-2003; 2003US-0454536P.  
PR 14-MAR-2003; 2003US-0455010P.  
PR 14-MAR-2003; 2003US-0455036P.  
PR 14-MAR-2003; 2003US-0455054P.  
PR 14-MAR-2003; 2003US-0455082P.  
PR 17-MAR-2003; 2003US-0455191P.  
PR 17-MAR-2003; 2003US-0455192P.  
PR 17-MAR-2003; 2003US-0455334P.  
PR 17-MAR-2003; 2003US-0455335P.  
PR 17-MAR-2003; 2003US-0455343P.  
XX  
XX  
PA (AFFI-) AFFINIUM PHARM INC.  
XX Edwards A, Dharansi A, Vedadi M, Domagala M, Nethery K;  
PI Mansoury K, FINDER B, Alam MZ, Ng I, Virag C, Houston S;  
PI McDonald M, Buzadzija K;  
XX  
XX WPI: 2004-400642/37.  
DR N-PSDB; ADO25482.  
XX  
XX Bacterial polypeptide composition useful for treating bacterial  
PT infection, has isolated, recombinant bacterial polypeptide such as GTP-  
PT binding protein Era from *Pseudomonas aeruginosa* or *adenylosuccinate lyase*  
PT from *Enterococcus faecalis*.  
XX  
XX Claim 41; SEQ ID NO 158; 566pp; English.  
XX  
XX This invention relates to the identification of novel protein targets for  
CC the development of antimicrobial drugs against pathogenic bacteria.  
CC Specifically, it refers to recombinant proteins derived from  
CC *Staphylococcus aureus*, *Helicobacter pylori*, *Streptococcus pneumoniae*,  
CC *Escherichia coli*, *Enterococcus faecalis* or *Pseudomonas aeruginosa*. The  
CC present invention describes providing a three-dimensional structure for the  
CC these crystallised proteins to identify a potential modulator for the  
CC prevention or treatment of microbial diseases. Furthermore, contacting a  
CC protein with a modulator can be useful for assaying protein activity and  
CC hence its viability in drug composition or vaccine. Accordingly, such  
CC compositions can be useful for treating bacterial infections, developing  
CC antibacterial agents useful as food preservatives or treating food  
CC products to eliminate potential pathogens. This polypeptide sequence is a  
CC bacterial protein target of the invention.  
XX  
XX Sequence 454 AA;  
SQ  
Query Match 11.7%; Score 84; DB 8; Length 454;  
Best Local Similarity 26.5%; Pred. No. 2.3;  
Matches 26; Conservative 15; Mismatches 35; Indels 22; Gaps 2;  
QY 33 GIFAFIPSPFLYKLLQWYRKNKKEQIRHQIELGLLSYGAGVASPLLNVAHPGS 92  
DB 165 GVHAEPTTFGVKMLWYTEMQRLQRFKQVREIEVGKMSGAVG-----TFANIPPE 216  
QY 93 VISATPIYKGPCTGVPNSRLQLQITSGTAENTRIILNHD 130  
DB 217 IESYVCKHLG-----IGTAPVSTQTLQRD 240  
RESULT 6  
ADO25483  
ID ADO25483 standard; protein; 454 AA.  
XX  
XX ADO25483;  
AC  
XX  
XX  
DT 12-AUG-2004 (first entry)  
XX  
XX S\_aureus adenylosuccinate lyase purB protein Seq158.  
XX  
XX antimicrobial; microbial disease; drug composition; vaccine;  
XX bacterial infection; antibacterial; food preservative.  
XX  
XX Staphylococcus aureus.  
OS  
XX  
XX W02004041854-A2.  
PN  
XX  
XX 21-MAY-2004.  
PD  
XX  
XX  
XX  
XX 05-NOV-2003; 2003WO-CA001671.  
XX  
XX  
XX 05-NOV-2002; 2002US-0423757P.  
PR 05-NOV-2002; 2002US-0423758P.  
PR 05-NOV-2002; 2002US-0423791P.  
PR 05-NOV-2002; 2002US-0423832P.  
PR 05-NOV-2002; 2002US-0423875P.  
PR 05-NOV-2002; 2002US-0423915P.  
PR 06-NOV-2002; 2002US-0424362P.  
PR 06-NOV-2002; 2002US-0424367P.  
PR 06-NOV-2002; 2002US-0424370P.  
PR 06-NOV-2002; 2002US-0424373P.  
PR 06-NOV-2002; 2002US-0424376P.  
PR 06-NOV-2002; 2002US-0424389P.  
PR 07-NOV-2002; 2002US-0424502P.  
PR 07-NOV-2002; 2002US-0424651P.  
PR



19-JUN-2003 (first entry)  
 Protein encoded by Prokaryotic essential gene #28959.  
 Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 Staphylococcus haemolyticus.  
 WO200277183-A2.  
 03-OCT-2002.  
 21-MAR-2002; 2002WO-US009107.  
 21-MAR-2001; 2001US-00815242.  
 06-SEP-2001; 2001US-00948993.  
 25-OCT-2001; 2001US-0342923P.  
 08-FEB-2002; 2002US-00072851.  
 06-MAR-2002; 2002US-0362699P.  
 (ELIT-) ELITRA PHARM INC.  
 Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,  
 Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 WPI; 2003-029926/02.  
 N-PSDB; ACA47302.  
 New antisense nucleic acids, useful for identifying proteins or screening  
 for homologous nucleic acids required for cellular proliferation to  
 isolate candidate molecules for rational drug discovery programs.  
 Claim 25; SEQ ID NO 71356; 1766pp; English.  
 The invention relates to an isolated nucleic acid comprising any one of  
 the 6213 antisense sequences given in the specification where expression  
 of the nucleic acid inhibits proliferation of a cell. Also included are:  
 (1) a vector comprising a promoter operably linked to the nucleic acid  
 encoding a polypeptide whose expression is inhibited by the antisense  
 nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 polypeptide or its fragment whose expression is inhibited by the  
 antisense nucleic acid; (4) an antibody capable of specifically binding  
 the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 proliferation or the activity of a gene in an operon required for  
 proliferation; (7) identifying a compound that influences the activity of  
 the gene product or that has an activity against a biological pathway  
 required for proliferation, or that inhibits cellular proliferation; (8)  
 identifying a gene required for cellular proliferation or the biological  
 pathway in which a proliferation-required gene or its gene product lies  
 or a gene on which the test compound that inhibits proliferation of an  
 organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 compound's activity; (11) a culture comprising strains in which the gene  
 product is overexpressed or underexpressed; (12) determining the extent  
 to which each of the strains is present in a culture or collection of  
 strains; or (13) identifying the target of a compound that inhibits the  
 proliferation of an organism. The antisense nucleic acids are useful for  
 identifying proteins or screening for homologous nucleic acids  
 required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
*K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 the target prokaryotic essential genes. Note: The sequence data for this  
 in electronic format directly from WIPO at  
 ftp.wipo.int/pub/published\_pct\_sequences

Query Match 11.2%; Score 80.5; DB 6; Length 431;  
 Best Local Similarity 34.0%; Pred. NO. 5.4;  
 Matches 17; Conservative 13; Mismatches 19; Indels 1; Gaps 1;  
 33 GIFAFIFSLYKLLQWYNRKSKKKKEQIREQIELGLLSYGAGV-ASLP 81

RESULT 10  
 AEU42716  
 ID ABU42716 standard; protein; 431 AA.  
 AC AC  
 ABU42716;  
 DT 19-JUN-2003 (first entry)  
 XX  
 DE Protein encoded by Prokaryotic essential gene #28243.  
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 OS Staphylococcus epidermidis.  
 XX  
 PN WO200277183-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 21-MAR-2002; 2002WO-US009107.  
 XX  
 PR 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.  
 Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,  
 Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 WPI; 2003-029926/02.  
 N-PSDB; ACA46586.  
 New antisense nucleic acids, useful for identifying proteins or screening  
 for homologous nucleic acids required for cellular proliferation to  
 isolate candidate molecules for rational drug discovery programs.  
 Claim 25; SEQ ID NO 70640; 1766pp; English.  
 The invention relates to an isolated nucleic acid comprising any one of  
 the 6213 antisense sequences given in the specification where expression  
 of the nucleic acid inhibits proliferation of a cell. Also included are:  
 (1) a vector comprising a promoter operably linked to the nucleic acid  
 encoding a polypeptide whose expression is inhibited by the antisense  
 nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 polypeptide or its fragment whose expression is inhibited by the  
 antisense nucleic acid; (4) an antibody capable of specifically binding  
 the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 proliferation or the activity of a gene in an operon required for  
 proliferation; (7) identifying a compound that influences the activity of  
 the gene product or that has an activity against a biological pathway  
 required for proliferation, or that inhibits cellular proliferation; (8)  
 identifying a gene required for cellular proliferation or the biological  
 pathway in which a proliferation-required gene or its gene product lies  
 or a gene on which the test compound that inhibits proliferation of an  
 organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 compound's activity; (11) a culture comprising strains in which the gene  
 product is overexpressed or underexpressed; (12) determining the extent  
 to which each of the strains is present in a culture or collection of  
 strains; or (13) identifying the target of a compound that inhibits the  
 proliferation of an organism. The antisense nucleic acids are useful for  
 identifying proteins or screening for homologous nucleic acids required  
 for cellular proliferation to isolate candidate molecules for rational  
 drug discovery programs, or for screening homologous nucleic acids  
 required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
*K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 the target prokaryotic essential genes. Note: The sequence data for this  
 patent did not form part of the printed specification, but was obtained  
 in electronic format directly from WIPO at  
 ftp.wipo.int/pub/published\_pct\_sequences

CC in electronic format directly from WIPO at  
CC [ftp.wipo.int/pub/published\\_pct\\_sequences](ftp.wipo.int/pub/published_pct_sequences)

XX  
SQ Sequence 431 AA;

Query Match      Score 80.5;    DB 6;    Length 431;  
Best Local Similarity    34.0%;    Pred. No. 5.4;

Matches 17; Conservative 13; Mismatches 19; Indels 1;

33 CTEAFTCEEI YKI I OEWXNBKSNKKRKEOTPBOTIFCII SVCAICV - AELP 91

QY 33 GIFAPIFSFLYKLLQWYNRKSQNKRRKEQIREQIELGLLSYGAGV-ASLP 81

[illegible]

## RESULT 11

RESOLUT  
ABP39818

ABP39818  
ID ABP39818 standard; protein; 458 AA.

AC 39818:

24-JUL-2002 (first entry)

PT binding protein Bxa from Pseudomonas aeruginosa or adenylosuccinate lyase  
PT from Enterococcus faecalis.

PS Claim 41; SEQ ID NO 160; 566pp; English.

XX This invention relates to the identification of novel protein targets for  
CC the development of antimicrobial drugs against pathogenic bacteria.  
CC Specifically, it refers to recombinant proteins derived from  
CC Staphylococcus aureus, Helicobacter pylori, Streptococcus pneumoniae,  
CC Escherichia coli, Enterococcus faecalis or Pseudomonas aeruginosa. The  
CC present invention describes providing a three-dimensional structure for  
CC these crystallised proteins to identify a potential modulator for the  
CC prevention or treatment of microbial diseases. Furthermore, contacting a  
CC protein with a modulator can be useful for assaying protein activity and  
CC hence its viability in drug composition or vaccine. Accordingly, such  
CC compositions can be useful for treating bacterial infections, developing  
CC antibacterial agents useful as food preservatives or treating food  
CC products to eliminate potential pathogens. This polypeptide sequence is a  
CC bacterial protein target of the invention.

XX Sequence 454 AA;

Query Match 11.0%; Score 79; DB 8; Length 454;

Best Local Similarity 25.5%; Pred. No. 8.6;

Matches 25; Conservative 16; Mismatches 35; Indels 22; Gaps 2;

QY 33 GIFAFIFSLYKLOWNRKSNKKKEQIREQIREGLLSYGAGVASPLLNVAHNPQS 92

DB 165 GVHAPFTTGVQWALMTTEPNRLQRFKQREIEVGRMGAVG-----TFANIPPE 216

QY 93 VISATPIYKPGCTGVNSRLLOITSGTAENTRLNHD 130

DB 217 IESYVCKHLG-----IGTAPVSIQTQORD 240

RESULT 13

ABB48477

ID ABB48477 standard; protein; 391 AA.

AC ABB48477;

DT 05-FEB-2002 (first entry)

XX Listeria monocytogenes protein #1181.

XX Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;

KW vitamin B12; bacterial infection; disease.

XX Listeria monocytogenes.

OS WO200177335-A2.

PN 18-OCT-2001.

PF 11-APR-2001; 2001WO-FR001118.

PR 11-APR-2000; 2000FR-00004629.

PA (INSP ) INST PASTEUR.

XX Buchrieser C, Frangeul L, Couve E, Rueniok C, Fsihi H, Dehoux P;  
PI Dussauget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;  
PI Daniels J, Goebel W, Kref J, Kuhn M, Ng E, Vazquez-Boland JA;  
PI Dominguez-Bernal G, Garrido-Garcia P, Rierrez-Martinez A, Amend A;  
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;  
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;  
PI Maduenio E, De Pablo B, Wehland J, Kaerst U, Entian K, Hauf J;  
PI Rose M, Voss H;

XX WPI; 2002-010914/01.

XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment  
PT and prevention of Listeria and related bacterial infections, and related

PT polypeptides.

PS Claim 6; SEQ ID NO 1182; 192pp; French.

XX The present invention relates to the genome sequence of Listeria  
CC monocytogenes EGD-a (see ABA03041). The genome sequence and fragments of  
CC it are useful for selecting probes and primers for detecting genes in L.  
CC monocytogenes and related organisms, and for studying genetic  
CC polymorphisms and other genomes. The present sequence is a protein  
CC encoded by the genome sequence of the present invention. Proteins  
CC expressed from the genome sequence are useful for raising specific  
CC antibodies, identification of L. monocytogenes and related organisms, and  
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin  
CC B12. The genome sequence and proteins encoded by it are also useful for  
CC selecting compounds that regulate gene expression and cell replication  
CC and modulate L. monocytogenes-related diseases. In addition, the genome  
CC sequence and proteins encoded by it are useful in pharmaceutical and  
CC vaccine compositions for the treatment or prevention of infections by L.  
CC monocytogenes and related organisms. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 391 AA;

Query Match 10.8%; Score 78; DB 5; Length 391;

Best Local Similarity 28.3%; Pred. No. 9.1;

Matches 30; Conservative 14; Mismatches 24; Indels 38; Gaps 5;

QY 56 KKRKEQIREQIREGL-----LSYGAGVASPLLNVAHNPQS-----VISATPIY 100

DB 79 KKAABESREQIREALKSDMVFVTAGMGCGTGAAPVIAQIAKENGALTGVVTRPFGF 138

QY 101 KGP-----CTG-----VPNSRLLOITSGTAENTRIL 127

DB 139 EGPKEKTKOALGTGTEAKGAVDTLIVIPNRLLOI-----VDKNTPLM 180

RESULT 14

ABU32700

ID ABU32700 standard; protein; 391 AA.

AC ABU32700;

DT 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #18227.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS Listeria monocytogenes.

XX WO200277183-A2.

PN 03-OCT-2002.

PF 21-MAR-2002; 2002WO-US009107.

PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0363699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Hasebeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA36570.

XX New antisense nucleic acids, useful for identifying proteins or screening



PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 60624; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 391 AA;

Query Match 10.8%; Score 78; DB 6; Length 391;  
Best Local Similarity 28.3%; Pred. No. 9.1; Indels 24; Gaps 5;  
Matches 30; Conservative 14; Mismatches 38; Gaps 5;  
QY 56 KKRQIRREQIRGL-----LSYGAGVASPLLNIAHNPQS-----VISATPIY 100  
DB 79 KKAESRQIRSEALKGSDFVTGACGGGTGTAAPVIAQIAKENGALTGVVTRPFGF 138  
QY 101 KGP-----CTG-----VPSRLQLQITSGTAEENTRIL 127  
DB 139 EGPRTKQALGTGAEMKAVDTLIVPNDRLQLI-----VDKNTPL 180

RESULT 15  
ABU26499  
ID ABU26499 standard; protein; 339 AA.  
XX  
AC ABU26499;  
XX  
DT 19-JUN-2003 (first entry)  
XX  
DE Protein encoded by Prokaryotic essential gene #12026.  
XX  
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
OS Campylobacter jejuni.  
XX  
PN WO200277183-A2.  
XX  
PD 03-OCT-2002.  
XX  
PP 21-MAR-2002; 2002WO-US009107.  
XX  
PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.  
PR 25-OCT-2001; 2001US-0342923P.  
PR 08-FEB-2002; 2002US-00072851.  
PR 06-MAR-2002; 2002US-0362699P.  
XX  
PA (ELIT-) ELITRA PHARM INC.  
XX  
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
DR WPI: 2003-029926/02.  
DR N-PSDB; ACA30369.  
XX  
PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX  
PS Claim 25; SEQ ID NO 54423; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of  
XX the 6213 antisense sequences given in the specification where expression  
XX of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 339 AA;

Query Match 10.8%; Score 77.5; DB 6; Length 339;  
Best Local Similarity 28.4%; Pred. No. 8.6;  
Matches 31; Conservative 14; Mismatches 31; Indels 33; Gaps 5;  
QY 48 WYNRKSK-----KKRK-----EQIREQELGLSYGAGVASPLLNIAHNP 91  
DB 61 WLDKEKNILNQBALKNPKLLSIIDKINDELEFGRFYA-----VKILAHNEK 112  
QY 92 SVISATPIYKPGCTGVPSRLQLQITSGTAEENTRILNHDGRNPDGSINV 140  
DB 113 TIVSATDI-----SDEKNERLASMGVAH-----LAHEIRNPIGSI 152

Search completed: November 15, 2004, 14:54:18  
Job time : 164 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:51:55 ; Search time 141 Seconds  
(without alignments)

351.310 Million cell updates/sec

Title: US-09-943-002-14

Perfect score: 720

Sequence: 1 MGQRHSIVQPPAPPNAFVE.....BENTRILNHDGRNPDGSINV 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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19: /cgm2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pap:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description          |
|------------|-------|-------------|--------|-------|----------------------|
| 1          | 720   | 100.0       | 140    | 9     | US-09-943-002-14     |
| 2          | 84    | 11.7        | 431    | 9     | US-09-815-242-5406   |
| 3          | 84    | 11.7        | 431    | 9     | US-09-815-242-12488  |
| 4          | 84    | 11.7        | 431    | 15    | US-10-282-122A-44335 |
| 5          | 84    | 11.7        | 636    | 15    | US-10-425-114-45755  |
| 6          | 80.5  | 11.2        | 376    | 17    | US-10-739-930-8926   |
| 7          | 80.5  | 11.2        | 431    | 15    | US-10-282-122A-70640 |
| 8          | 80.5  | 11.2        | 431    | 15    | US-10-282-122A-71356 |
| 9          | 80.5  | 11.2        | 756    | 15    | US-10-424-599-200688 |
| 10         | 80.5  | 11.2        | 760    | 15    | US-10-425-114-39701  |
| 11         | 79.5  | 11.0        | 539    | 17    | US-10-425-115-290480 |
| 12         | 79.5  | 11.0        | 544    | 15    | US-10-425-114-43526  |
| 13         | 78.5  | 10.9        | 419    | 15    | US-10-437-963-183058 |

|    |      |      |      |      |    |                      |                    |
|----|------|------|------|------|----|----------------------|--------------------|
| 14 | 10.8 | 78   | 10.8 | 325  | 14 | US-10-369-493-10884  | Sequence 10884, A  |
| 15 | 78   | 10.8 | 10.8 | 391  | 15 | US-10-282-122A-60624 | Sequence 60624, A  |
| 16 | 77.5 | 10.8 | 10.8 | 339  | 15 | US-10-282-122A-54423 | Sequence 54423, A  |
| 17 | 77.5 | 10.8 | 10.8 | 606  | 15 | US-10-425-114-54999  | Sequence 54999, A  |
| 18 | 77.5 | 10.8 | 10.8 | 654  | 14 | US-10-369-493-5059   | Sequence 5059, Ap  |
| 19 | 75.5 | 10.5 | 10.5 | 1220 | 9  | US-09-801-368-332    | Sequence 22082, A  |
| 20 | 75.5 | 10.5 | 10.5 | 1220 | 14 | US-10-369-493-20882  | Sequence 149924, A |
| 21 | 75   | 10.4 | 10.4 | 601  | 16 | US-10-437-963-149924 | Sequence 654, App  |
| 22 | 75   | 10.4 | 10.4 | 892  | 15 | US-10-408-765A-654   | Sequence 53999, A  |
| 23 | 74.5 | 10.3 | 10.3 | 456  | 15 | US-10-425-114-53999  | Sequence 6678, Ap  |
| 24 | 74.5 | 10.3 | 10.3 | 498  | 9  | US-09-738-626-6678   | Sequence 150408, A |
| 25 | 74   | 10.3 | 10.3 | 289  | 15 | US-10-424-599-150408 | Sequence 4998, Ap  |
| 26 | 74   | 10.3 | 10.3 | 468  | 14 | US-10-369-493-4998   | Sequence 59396, A  |
| 27 | 73   | 10.1 | 10.1 | 262  | 15 | US-10-282-122A-59396 | Sequence 41480, A  |
| 28 | 73   | 10.1 | 10.1 | 307  | 15 | US-10-425-114-41480  | Sequence 303682, A |
| 29 | 73   | 10.1 | 10.1 | 359  | 17 | US-10-425-115-302682 | Sequence 316899, A |
| 30 | 73   | 10.1 | 10.1 | 451  | 17 | US-10-425-115-312699 | Sequence 51670, A  |
| 31 | 73   | 10.1 | 10.1 | 456  | 15 | US-10-425-114-51670  | Sequence 11, Appl  |
| 32 | 73   | 10.1 | 10.1 | 766  | 15 | US-10-471-449-11     | Sequence 274608, A |
| 33 | 72   | 10.0 | 10.0 | 163  | 17 | US-10-425-115-274608 | Sequence 701, App  |
| 34 | 72   | 10.0 | 10.0 | 649  | 14 | US-10-310-154-701    | Sequence 2982, Ap  |
| 35 | 72   | 10.0 | 10.0 | 687  | 14 | US-10-104-047-2982   | Sequence 190895, A |
| 36 | 71.5 | 9.9  | 9.9  | 69   | 17 | US-10-425-115-190895 | Sequence 160666, A |
| 37 | 71.5 | 9.9  | 9.9  | 158  | 16 | US-10-437-963-160666 | Sequence 52165, A  |
| 38 | 71.5 | 9.9  | 9.9  | 210  | 15 | US-10-282-122A-52165 | Sequence 3051, Ap  |
| 39 | 71.5 | 9.9  | 9.9  | 241  | 15 | US-10-320-797-3051   | Sequence 20773, A  |
| 40 | 71.5 | 9.9  | 9.9  | 481  | 14 | US-10-369-493-20773  | Sequence 8, Appli  |
| 41 | 71.5 | 9.9  | 9.9  | 766  | 17 | US-10-487-421-8      | Sequence 158433, A |
| 42 | 71   | 9.9  | 9.9  | 449  | 16 | US-10-437-963-158433 | Sequence 125813, A |
| 43 | 71   | 9.9  | 9.9  | 645  | 16 | US-10-437-963-125813 | Sequence 142238, A |
| 44 | 71   | 9.9  | 9.9  | 707  | 16 | US-10-437-963-142238 | Sequence 9, Appli  |
| 45 | 70.5 | 9.8  | 9.8  | 360  | 14 | US-10-195-144-9      |                    |

#### ALIGNMENTS

#### RESULT 1

US-09-943-002-14  
; Sequence 14, Application US/09943002  
; Patent No. US20020045734A1  
; GENERAL INFORMATION:  
; APPLICANT: Duncan, Roy  
; TITLE OF INVENTION: NOVEL REOVIRUS-DERIVED PROTEINS AND USES THEREFOR  
; FILE REFERENCE: 78973-1C  
; CURRENT APPLICATION NUMBER: US/09/943,002  
; CURRENT FILING DATE: 2001-08-31  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 140  
; TYPE: PRT  
; ORGANISM: baboon reovirus  
US-09-943-002-14

Query Match 100.0%; Score 720; DB 9; Length 140;  
Best Local Similarity 100.0%; Pred. No. 3.7e-72;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |                                                           |     |
|----|-----|-----------------------------------------------------------|-----|
| QY | 1   | MGQRHSIVQPPAPPNAFVEIVSSSTGIIIAVGIPAFIFSLYKLLQWYNRKSKNRKKE | 60  |
| DB | 1   | MGQRHSIVQPPAPPNAFVEIVSSSTGIIIAVGIPAFIFSLYKLLQWYNRKSKNRKKE | 60  |
| QY | 61  | QIRQIEIGLLSYGAGVASLPLNVIANPGSVISATPIYKGPCTGVPSNRLLOITSGTA | 120 |
| DB | 61  | QIRQIEIGLLSYGAGVASLPLNVIANPGSVISATPIYKGPCTGVPSNRLLOITSGTA | 120 |
| QY | 121 | BENTRILNHDGRNPDGSINV                                      | 140 |
| DB | 121 | BENTRILNHDGRNPDGSINV                                      | 140 |

#### RESULT 2







QY 105 T--GVNSR-----LLQITSGTASEN 123  
DB 389 EPGVSSRSWFYBELLQATNGFSAQN 416

## RESULT 11

US-10-425-115-290480  
; Sequence 290480, Application US/10425115  
; Publication No. US20040214272A1

## GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

FILE REFERENCE: 38-21(53222)B

TITLE OF INVENTION: Plants

CURRENT APPLICATION NUMBER: US/10/425,115

FILE FILING DATE: 2003-04-28

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 290480

LENGTH: 539

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: MRT4577\_28005C.1.pap

US-10-425-115-290480

Query Match 11.0%; Score 79.5; DB 17; Length 539;  
Best Local Similarity 35.6%; Pred. No. 8.9; Indels 1; Gaps 1;  
Matches 21; Conservative 10; Mismatches 27

QY 81 PLLNVIAHNPVSGVISATPIYKGPCTGVNSRLLOITSGTAEENTRLNHGDR-NPDGSI 138

DB 8 PLLVNNHSPGVPVATPGEHGAAYDESSTLVDAASGTDESHRALADADVKNDDGDV 66

## RESULT 12

US-10-425-114-43526  
; Sequence 43526, Application US/10425114  
; Publication No. US20040034888A1

## GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E.

APPLICANT: Tabaska, Jack E.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(5313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 43526

LENGTH: 544

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: 700444335\_FLI.pap

US-10-425-114-43526

Query Match 11.0%; Score 79.5; DB 15; Length 544;  
Best Local Similarity 35.6%; Pred. No. 9; Indels 1; Gaps 1;  
Matches 21; Conservative 10; Mismatches 27

QY 81 PLLNVIAHNPVSGVISATPIYKGPCTGVNSRLLOITSGTAEENTRLNHGDR-NPDGSI 138

DB 13 PLLVNNHSPGVPVATPGEHGAAYDESSTLVDAASGTDESHRALADADVKNDDGDV 71

## RESULT 13

US-10-437-963-183058

; Sequence 183058, Application US/10437963  
; Publication No. US20040123343A1

## GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 183058

LENGTH: 419

TYPE: PRT

ORGANISM: Oryza sativa

FEATURE:

OTHER INFORMATION: Clone ID: PAT\_MRT4530\_80186C.1.pap

US-10-437-963-183058

Query Match 10.9%; Score 78.5; DB 16; Length 419;  
Best Local Similarity 23.0%; Pred. No. 8.3; Indels 41; Gaps 7;  
Matches 32; Conservative 22; Mismatches 44

QY 13 PPNAPVEIVSSSTGIITAVGIFAFIPFLYKLLWYNRKSNKKKQIREQI--ELGL 70

DB 239 PPPIAHLHAKA-----IMELWYNNNGYKVKYMBESRSNOGIMEEDSV 281

QY 71 LSVGAGVASLPILNVIAHNPVSGVISATPIYKGPCTGVNSRLLOI-----TSGTAEN 123

DB 282 ISNGGREBEV-----VWANGSGGKVVQVQLQRNPFGEVQGLEQN 333

QY 124 TRIL-----NHDGRNPDG 136

DB 334 -RVLIQETISQNHARDAG 351

## RESULT 14

US-10-369-493-10884

; Sequence 10884, Application US/10369493

; Publication No. US20030233675A1

## GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 10884

LENGTH: 325

TYPE: PRT

ORGANISM: Sphingomonas aromaticivorans

US-10-369-493-10884

Query Match 10.8%; Score 78; DB 14; Length 325;  
Best Local Similarity 36.7%; Pred. No. 6.7; Indels 0; Gaps 0;  
Matches 18; Conservative 7; Mismatches 24

QY 90 PGVSISATPIYKGPCTGVNSRLLOITSGTAEENTRLNHGDRNPDGSI 138

DB 92 PGAAIHAQPSYRTHGEMIPRSRPVALTTLTGTEATILANPNPDGRI 140

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RESULT 15
US-10-282-122A-60624
; Sequence 60624, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60624
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-10-282-122A-60624

Query Match      10.8%; Score 78; DB 15; Length 391;
Best Local Similarity 28.3%; Pred. No. 8.6;
Matches 30; Conservative 14; Mismatches 24; Indels 38; Gaps 5;

QY      56 KKKKEIQIREQIELGL-----LSYCGAGVASLPLLVIAHNPQS----VISATPIY 100
      |||:|||||:
Db      79 KKAEEESREIQIEALKGSDMVFVTAGGGGTGTAAPVIAQIAKEMGALTGVVTRPFGP 138
      |||:|||||:

QY      101 KGP-----CTG-----VPSNRLLQITSGTAENTRIL 127
      |||:|||||:
Db      139 EGPKRTKQALTGTTEAMKEAVDTLIVIPNDRLLOI-----VDKNTPML 180
      |||:|||||:

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Search completed: November 15, 2004, 15:01:30  
Job time : 142 secs

| Result No. | Score | Query Match | Length | DB | ID     | Description         |
|------------|-------|-------------|--------|----|--------|---------------------|
| 1          | 84    | 11.7        | 431    | 2  | C89979 | adenylosuccinate 1  |
| 2          | 83    | 11.5        | 167    | 2  | D70401 | phosphoribosylamin  |
| 3          | 78    | 10.8        | 255    | 2  | A75507 | conserved hypothet  |
| 4          | 78    | 10.8        | 391    | 2  | AH1328 | cell-division init  |
| 5          | 78    | 10.8        | 392    | 2  | AH1699 | cell-division init  |
| 6          | 77.5  | 10.8        | 339    | 2  | A81351 | signal transduction |
| 7          | 77.5  | 10.8        | 654    | 2  | C87791 | protein B0207.12 [  |
| 8          | 76    | 10.6        | 298    | 2  | T36900 | probable integral   |
| 9          | 76    | 10.6        | 1477   | 2  | T19534 | protein-tyrosine k  |
| 10         | 75.5  | 10.5        | 427    | 2  | S19338 | hypothetical prote  |
| 11         | 75.5  | 10.5        | 1220   | 2  | S48387 | SLN1 protein - yea  |
| 12         | 75    | 10.4        | 399    | 1  | S76745 | hypothetical prote  |
| 13         | 74.5  | 10.3        | 305    | 2  | D90031 | hypothetical prote  |
| 14         | 74.5  | 10.3        | 359    | 2  | T36781 | probable gluconate  |
| 15         | 74    | 10.3        | 433    | 2  | S05654 | ND3 intron protein  |
| 16         | 74    | 10.3        | 468    | 2  | T33857 | hypothetical prote  |
| 17         | 74    | 10.3        | 599    | 2  | T15774 | hypothetical prote  |
| 18         | 73.5  | 10.2        | 256    | 2  | T45049 | hypothetical prote  |
| 19         | 73    | 10.1        | 443    | 2  | S11396 | gamma-aminobutyric  |
| 20         | 73    | 10.1        | 3036   | 2  | T18995 | hypothetical prote  |
| 21         | 72.5  | 10.1        | 120    | 2  | S07727 | NADH2 dehydrogenas  |
| 22         | 72.5  | 10.1        | 133    | 2  | T30474 | hypothetical prote  |
| 23         | 72.5  | 10.1        | 338    | 2  | T23260 | hypothetical prote  |
| 24         | 72.5  | 10.1        | 1677   | 2  | T46095 | hypothetical prote  |
| 25         | 72    | 10.0        | 453    | 2  | S11087 | gamma-aminobutyric  |
| 26         | 72    | 10.0        | 631    | 2  | D63750 | phosphotransferase  |
| 27         | 72    | 10.0        | 714    | 2  | AF2479 | ABC transporter AT  |
| 28         | 72    | 10.0        | 910    | 2  | A53137 | tyrosine kinase re  |
| 29         | 71.5  | 9.9         | 210    | 2  | G97235 | hypothetical prote  |



C:Genetics:  
A:Gene: pure  
C:Superfamily: phosphoribosylaminoimidazole carboxylase catalytic chain; phosphoribosyl  
C:Keywords: carbon-carbon lyase; carboxy-lyase; purine nucleotide biosynthesis  
P:3-136/Domain: phosphoribosylaminoimidazole carboxylase catalytic chain homology <PC>  
Query Match 11.5%; Score 83; DB 2; Length 167;  
Best Local Similarity 33.8%; Pred. No. 0.77;  
Matches 23; Conservative 15; Mismatches 28; Indels 2; Gaps 1;  
QY 5 HSTVQPPAPPPAFVETIVSSGIIITAVGIFAFIFSFYKLLQWYRKSKNK--KKKEQI 62  
DB 100 YSIQVQMPAGIVATVAIGNATNAGLLAVRLISIKYPEYAKLDDEYTEKLKRVAKGNEL 159  
QY 63 REQIELGL 70  
DB 160 QKEVENGI 167  
RESULT 3  
A:Map position: 1  
C:Superfamily: hypothetical protein - Deinococcus radiodurans (strain R1)  
conserved hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: A75507  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M.; Shen, O.; Eisen, J.A.; Heidberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; White, O.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896; PMID:10567266  
A:Accession: A75507  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-255 <WHI>  
A:Cross-references: UNIPROT:Q9RWX1; GB:AE001912; GB:AE000513; NID:96458228; PIDN:AAF1011  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DR0544  
A:Map position: 1  
C:Superfamily: hypothetical protein HI0902  
Query Match 10.8%; Score 78; DB 2; Length 255;  
Best Local Similarity 27.3%; Pred. No. 3.9;  
Matches 30; Conservative 14; Mismatches 42; Indels 24; Gaps 3;  
QY 22 VSSSTGIIIVGIFAFIFSL-----YKLLQWYRKSKNKKEQIREQIEL----- 68  
DB 94 VGSFGLVLPARAVATVFALLFYSAYNLL-----RGLKREVEREPKLVPPAMTPA 146  
QY 69 ---GLLSYGAGVASLPLLVIAHNPVSGVTSATPIYKGPCTGVPSRLAQ 114  
DB 147 GWSGLLGIGGTQVQVPLVNLNMGHPQIRQAIATSTFIMGLTAVGNALVTQ 196  
RESULT 4  
AH1328  
cell-division initiation protein FtsZ homolog ftsZ [imported] - Listeria monocytogenes  
C:Species: Listeria monocytogenes  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AH1328  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kreitz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M.; Shen, O.; Eisen, J.A.; Heidberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; White, O.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Fraser, C.M.  
A:Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AH1328  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-391 <GLA>

A:Cross-references: UNIPROT:Q8YSM5; GB:NC\_003210; PIDN:CAD00110.1; PID:g16411502; GSPDB  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: ftsZ  
C:Superfamily: cell division protein ftsZ  
Query Match 10.8%; Score 78; DB 2; Length 391;  
Best Local Similarity 28.3%; Pred. No. 6.3;  
Matches 30; Conservative 14; Mismatches 24; Indels 38; Gaps 5;  
QY 56 KKRKEQIREQIELGL-----LSYGAGVASLPLLVIAHNPVSGVTSATPIY 100  
DB 79 KKAABESREQIEALKGDVMTAGMGCGTGTGAAPVIAQIAKEMGALTGVGVTRPPFGF 138  
QY 101 KGP-----CTG-----VPNSRLLOITSGTAENTRIL 127  
DB 139 EGPKRTKQALTGTETAMKEAVDTLIVIPNDRLLQI-----VDKNTPLM 180  
RESULT 5  
AH1699  
cell-division initiation protein FtsZ homolog ftsZ [imported] - Listeria innocua (strain  
C:Species: Listeria innocua  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AH1699  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kreitz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M.; Shen, O.; Eisen, J.A.; Heidberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; White, O.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Fraser, C.M.  
A:Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AH1699  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-392 <GLA>  
A:Cross-references: UNIPROT:Q929Y5; GB:AL592022; PIDN:CAC97368.1; PID:g16414652; GSPDB:  
A:Experimental source: strain Clip11262  
C:Genetics:  
A:Gene: ftsZ  
C:Superfamily: cell division protein ftsZ  
Query Match 10.8%; Score 78; DB 2; Length 392;  
Best Local Similarity 28.3%; Pred. No. 6.4;  
Matches 30; Conservative 14; Mismatches 24; Indels 38; Gaps 5;  
QY 56 KKRKEQIREQIELGL-----LSYGAGVASLPLLVIAHNPVSGVTSATPIY 100  
DB 79 KKAABESREQIEALKGDVMTAGMGCGTGTGAAPVIAQIAKEMGALTGVGVTRPPFGF 138  
QY 101 KGP-----CTG-----VPNSRLLOITSGTAENTRIL 127  
DB 139 EGPKRTKQALTGTETAMKEAVDTLIVIPNDRLLQI-----VDKNTPLM 180  
RESULT 6  
AH1351  
signal transduction histidine kinase Cj0793 [imported] - Campylobacter jejuni (strain N  
C:Species: Campylobacter jejuni  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C:Accession: AB1351  
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Baeham, D.; Chiller, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barre, Nature 403, 663-668, 2000  
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hy  
A:Reference number: AB1250; MUID:20150912; PMID:10688204  
A:Accession: AB1351  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-339 <PAR>  
A:Cross-references: UNIPROT:Q9PPC6; GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB730;  
A:Experimental source: serotype O2, strain NCTC 11168

## C;Genetics:

A;Gene: Cj0793

Query Match 10.8%; Score 77.5; DB 2; Length 339;  
Best Local Similarity 28.4%; Pred. No. 6;  
Matches 31; Conservative 14; Mismatches 31; Indels 33; Gaps 5;

QY 48 WYNRKSKN-----KKKK-----EQIREQIELGLLSYGAGVASLPLLVIAHNP 91

DB 61 WILDEKNIILQNEALKNPKLLSIISLKDIRELEPEGRFYA-----VKIIAHNEK 112

QY 92 SVLSATPIYKPGCTGVNSKLLQITSGTAENTRILNHDGNSINV 140

DB 113 TIVSATDI-----SDEKRNRLASMGVAAH-----LAHEIRNPTGISL 152

## RESULT 7

C87791

protein B0207.12 (imported) - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001

C;Accession: C87791

R;Anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A;Reference number: A75000; PMID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C\_ele

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A;Accession: C87791

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-654 &lt;STO&gt;

A;Cross-references: GB;chr\_1; PIDN:BA852465.1; PID:g1943811; GSPDB:GN00019; CESP:B0207.1

A;Note: Similar to ligand-gated ionic channel

## C;Genetics:

A;Gene: B0207.12

A;Map position: 1

Query Match 10.8%; Score 77.5; DB 2; Length 654;  
Best Local Similarity 29.9%; Pred. No. 13;  
Matches 26; Conservative 16; Mismatches 26; Indels 19; Gaps 5;

QY 14 PPNAPVEIVSSSTGIITAVGIFAFIPISFL--YKLLWYNRKS---KNKKKEQI----- 62

DB 532 PPSVIKADVNVIGVCL-----AFIGALLEYAVVNYGKEFLRKEKKKTRIDDCVCP 586

QY 63 --REQIELGLLSYGAGVASLPLLVIA 87

DB 587 SDRPPLRLDSAY-RSVKRLPIIKRIS 612

## RESULT 8

T36900

probable integral membrane transport protein - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: T36900

R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, July 1999

A;Reference number: Z21574

A;Accession: T36900

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-298 &lt;SEE&gt;

A;Cross-references: UNIPROT:Q9X9Y6; EMBL:AL096743; PIDN:CAB46387.1; GSPDB:GN000070; SCORE

A;Experimental source: strain A3(2)

## C;Genetics:

A;Gene: SC0DB:SCI7.04C

C;Superfamily: maltose transport protein malG

Query Match 10.6%; Score 76; DB 2; Length 298;  
Best Local Similarity 34.8%; Pred. No. 7.3;  
Matches 23; Conservative 14; Mismatches 21; Indels 8; Gaps 3;

QY 29 IIAVGIFAFIFS---FLYKLLWYNRKSNNK-----KRKEQIREQIELGLLSYGAGVASLP 81  
DB 217 LIAVGSPAFVHSWNHFLPALM-PLNNQSKOTIPVGLNSLSMSADSVLDGALAAGGIVAAP 275

QY 82 LNVIA 87

DB 276 VVIVFA 281

## RESULT 9

T18534

protein-tyrosine kinase - Hydra vulgaris

N;Alternate names: insulin-like receptor protein

C;Species: Hydra vulgaris

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T18534

R;Steele, R.E.; Mai, N.H.; Lieu, P.; Shenk, M.A.

submitted to the EMBL Data Library, May 1995

A;Description: An insulin-like receptor gene is expressed in dividing epithelial cells

A;Reference number: Z18954

A;Accession: T18534

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1477 &lt;STB&gt;

A;Cross-references: UNIPROT:Q25197; EMBL:M64612; PID:g858746; PID:AAA6820

A;Experimental source: adult polyp

C;Genetics:

A;Gene: HYK7

C;Superfamily: insulin receptor; protein kinase homology

Query Match 10.6%; Score 76; DB 2; Length 1477;  
Best Local Similarity 20.9%; Pred. No. 45;  
Matches 28; Conservative 25; Mismatches 31; Indels 50; Gaps 5;

QY 19 VEIVSSSTGIITAVGIFAFIPISFLYKLL-----QWYNRK-----SKNK 56

DB 982 IGIISAVSAVIVALLVFIILYMLHRKLEKDVQGVLYASVNPYMSKSYVIPPDEWELNR 1041

QY 57 KRKEQIREQIELGLLSYGAGVASLPLLVIAHNPVISATPIYKPGCTGVNSRLLOIT 116

DB 1042 EKIELIR---ELQGSGFM-----VFEGIAHGIGDHAEURVA 1075

QY 117 SGTAENTRILNHD 130

DB 1076 VKTTNENASI--HD 1087

## RESULT 10

S19338

hypothetical protein YCL011c - Yeast (Saccharomyces cerevisiae)

C;Species: Saccharomyces cerevisiae

C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Aug-2004

C;Accession: S19338

R;Oliver, S.G.; Anwar, R.; Brown, A.; Gent, M.E.; Indge, K.J.; James, C.M.; Stateva, L.

submitted to the Protein Sequence Database, March 1992

A;Reference number: S19337

A;Accession: S19338

A;Molecule type: DNA

A;Residues: 1-427 &lt;OLI&gt;

A;Cross-references: UNIPROT:P25555; EMBL:X59720; NID:g1907116; PIDN:CAA42348.1; PID:c26

C;Genetics:

A;Gene: SGD:GBP2

A;Cross-references: SGD:S0000517; MIPS:YCL011c

A;Map position: 3L

C;Superfamily: ribonucleoprotein repeat homology

C;Keywords: nucleus

F;123-188/Domain: ribonucleoprotein repeat homology &lt;RPM1&gt;

F;220-286/Domain: ribonucleoprotein repeat homology &lt;RRM2&gt;

F;350-416/Domain: ribonucleoprotein repeat homology &lt;RRM3&gt;

Query Match 10.5%; Score 75.5; DB 2; Length 427;  
Best Local Similarity 23.5%; Pred. No. 12;

probable gluconate permease - Streptomyces coelicolor (fragment)  
C:Species: Streptomyces coelicolor  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T36781  
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, July 1999  
A:Reference number: Z21614  
A:Accession: T36781



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 15, 2004, 14:32:21 / Search time 195 Seconds  
(without alignments)

413.089 Million cell updates/sec

Title: US-09-943-002-14

Perfect score: 720

Sequence: 1 MGRHSIVQPPPPNAPFVE.....EENTRLNHGDRNPDGSINV 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID           | Description        |
|------------|-------|-------------|--------|--------------|--------------------|
| 1          | 720   | 100.0       | 140    | 2 Q918V6     | Q918V6 baboon reov |
| 2          | 85.5  | 11.9        | 806    | 2 Q7QPH4     | Q7QPH4 giardia lam |
| 3          | 84    | 11.7        | 431    | 2 Q6G825     | Q6G825 staphylococ |
| 4          | 84    | 11.7        | 431    | 2 Q6GFE9     | Q6GFE9 staphylococ |
| 5          | 84    | 11.7        | 431    | 2 Q998X9     | Q998X9 staphylococ |
| 6          | 84    | 11.7        | 431    | 2 Q7A0G9     | Q7A0G9 staphylococ |
| 7          | 84    | 11.7        | 431    | 2 Q7A4Q3     | Q7A4Q3 staphylococ |
| 8          | 84    | 11.7        | 574    | 2 Q8DQ1      | Q8DQ1 synchococ    |
| 9          | 83    | 11.5        | 167    | 1 PURE AQUAE | Q67239 aquifex aeo |
| 10         | 82.5  | 11.5        | 536    | 2 Q22040     | Q22040 caenorhabdi |
| 11         | 82    | 11.4        | 734    | 2 Q7Q696     | Q7Q696 anopheles g |
| 12         | 80.5  | 11.2        | 431    | 2 Q8CR76     | Q8CR76 staphylococ |
| 13         | 79.5  | 11.0        | 443    | 2 Q6F2A9     | Q6F2A9 mesoplasma  |
| 14         | 79.5  | 11.0        | 1491   | 2 Q8C115     | Q8C115 m mus muscu |
| 15         | 79    | 11.0        | 633    | 2 Q8LP72     | Q8LP72 nicotiana t |
| 16         | 79    | 11.0        | 664    | 2 Q899Q9     | Q899Q9 clostridium |
| 17         | 78    | 10.8        | 255    | 2 Q9RWX1     | Q9RWX1 deinococcus |
| 18         | 78    | 10.8        | 391    | 2 Q8Y5M5     | Q8Y5M5 listeria mo |
| 19         | 78    | 10.8        | 391    | 2 Q71XY1     | Q71XY1 listeria mo |
| 20         | 78    | 10.8        | 391    | 2 AAT04834   | AAT04834 listeria  |
| 21         | 78    | 10.8        | 392    | 2 Q929Y5     | Q929Y5 listeria in |
| 22         | 77.5  | 10.8        | 339    | 2 Q9PPC6     | Q9PPC6 campylobact |
| 23         | 77.5  | 10.8        | 430    | 2 Q17369     | Q17369 caenorhabdi |
| 24         | 77.5  | 10.8        | 430    | 2 Q95Q97     | Q95Q97 caenorhabdi |
| 25         | 77    | 10.7        | 172    | 2 Q83314     | Q83314 enterococcu |
| 26         | 76.5  | 10.6        | 681    | 2 Q9FEW5     | Q9FEW5 arabidopsis |
| 27         | 76    | 10.6        | 187    | 2 Q8RF10     | Q8RF10 fusobacteri |
| 28         | 76    | 10.6        | 280    | 2 Q6YT74     | Q6YT74 oryza sativ |
| 29         | 76    | 10.6        | 280    | 2 BAC84718   | BAC84718 oryza sat |
| 30         | 76    | 10.6        | 298    | 2 Q9X9Y6     | Q9X9Y6 streptomyce |
| 31         | 76    | 10.6        | 308    | 2 Q8TQ34     | Q8TQ34 methanosarc |

|    |      |      |      |              |                     |
|----|------|------|------|--------------|---------------------|
| 32 | 76   | 10.6 | 765  | 2 Q7M857     | Q7M857 wolinnella s |
| 33 | 76   | 10.6 | 1477 | 1 HTK7 HYDAT | Q25197 hydra atten  |
| 34 | 75.5 | 10.5 | 427  | 1 GBP2 YEAST | P25555 saccharomyc  |
| 35 | 75.5 | 10.5 | 1220 | 1 SLN1 YEAST | P39928 saccharomyc  |
| 36 | 75   | 10.4 | 399  | 2 P74550     | P74550 synchococyt  |
| 37 | 75   | 10.4 | 481  | 2 Q7RG91     | Q7RG91 plasmodium   |
| 38 | 75   | 10.4 | 508  | 2 Q722R7     | Q722R7 bacillus ce  |
| 39 | 75   | 10.4 | 508  | 2 AAS43502   | AAS43502 bacillus   |
| 40 | 75   | 10.4 | 626  | 1 LPXB CHLCV | Q82123 chlamydomphi |
| 41 | 75   | 10.4 | 848  | 2 Q8P247     | Q8P247 methanosarc  |
| 42 | 75   | 10.4 | 892  | 2 Q9Y438     | Q9Y438 homo sapien  |
| 43 | 74.5 | 10.3 | 305  | 2 Q8G629     | Q8G629 staphylococ  |
| 44 | 74.5 | 10.3 | 305  | 2 Q8NV71     | Q8NV71 staphylococ  |
| 45 | 74.5 | 10.3 | 305  | 2 Q99RV2     | Q99RV2 staphylococ  |

ALIGNMENTS

RESULT 1

Q918V6 PRELIMINARY; PRT; 140 AA.  
AC Q918V6;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE Membrane fusion protein p15.  
OS Baboon reovirus.  
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.  
OX NCBI\_TaxID=75888;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Dawe S., Duncan R.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Shou J., Chen Z., Duncan R.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF406787; AAL01373.1; -  
SQ SEQUENCE 140 AA; 15222 MW; B02BDF37B6CE6075 CRC64;

Query Match 100.0%; Score 720; DB 2; Length 140;  
Best Local Similarity 100.0%; Pred. No. 1.7e-63;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGRHSIVQPPPPNAPFVEIVSSSTGIIIVGIFAFISFLYKLLQWYRKSKNKKRKE 60  
DB 1 MGRHSIVQPPPPNAPFVEIVSSSTGIIIVGIFAFISFLYKLLQWYRKSKNKKRKE 60  
QY 61 QIREQIEIGLLSYGAGVASLPLNLVIAHNPVSGVISATPIYKGPCTGVPNSRLQITSGTA 120  
DB 61 QIREQIEIGLLSYGAGVASLPLNLVIAHNPVSGVISATPIYKGPCTGVPNSRLQITSGTA 120  
QY 121 EENTRLNHGDRNPDGSINV 140  
DB 121 EENTRLNHGDRNPDGSINV 140  
QY 121 EENTRLNHGDRNPDGSINV 140  
DB 121 EENTRLNHGDRNPDGSINV 140

RESULT 2

Q7QPH4 PRELIMINARY; PRT; 806 AA.  
AC Q7QPH4;  
DT 01-MAR-2004 (TREMBlrel. 26, Created)  
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE GLP 41 11524 13944.  
OS Giardia lamblia ATCC 50803.  
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinales; Giardia.  
OX NCBI\_TaxID=184922;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WB C6;  
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,

4.

```

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=M50 / ATCC 700699;
RX MEDLINE=213111952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kaneshisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003363; BAB58070.1; --
DR FIC; C89979; C89979.
DR HSP; G9X010; IC3C.
DR GO; GO:0004018; F:adenylosuccinate lyase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0009152; P:purine ribonucleotide biosynthesis; IEA.
DR InterPro; IPR003031; D:crystallin.
DR InterPro; IPR000362; Fumarate_lyase.
DR InterPro; IPR008948; L-Aspartase-like.
DR Pfam; PF00206; Lyase 1; 1.
DR PRINTS; PR00145; DCRYSTALLIN.
DR PRINTS; PR00149; FUMATELYASE.
DR TIGRPFAMs; TIGR00928; purB; 1.
DR PROSITE; PS00163; FUMARATE_LYASES; 1.
DR Complete proteome; Lyase.
KW Complete proteome; Lyase.
SQ SEQUENCE 431 AA; 49603 MW; 493F79CBE814B9E5 CRC64;

Query Match 11.7%; Score 84; DB 2; Length 431;
Best Local Similarity 26.5%; Pred. No. 12;
Matches 26; Conservative 15; Mismatches 35; Indels 22; Gaps 2;

QY 33 GIFAIFSFYKLLQWYNRKSKKKRKEQIRIQEILGLLSYGAGVASPLLNVIHNPQS 92
DB 142 GVHAEPPTFGVKWALWYTEMQRNLQRFQVREIEVGKMSGAVG-----TFANIPPE 193

QY 93 VISATPIYKGPCTGVPSNRLQITSGTAENTRILNHD 130
DB 194 IESYVCKHLG-----IGTAPVSTQTLD 217

RESULT 7
QY 7A4Q3 PRELIMINARY; PRT; 431 AA.
AC Q7A4Q3;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Adenylosuccinate lyase.
GN Name=purB; OrderedLocusNames=SA1724;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=213111952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Kaneshisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003135; BAB42994.1; --
DR GO; GO:0016829; F:lyase activity; IEA.
DR InterPro; IPR003031; D:crystallin.
DR InterPro; IPR000362; Fumarate_lyase.
DR InterPro; IPR008948; L-Aspartase-like.
DR InterPro; IPR004769; Pur_lyase.
DR Pfam; PF00206; Lyase 1; 1.
DR PRINTS; PR00145; DCRYSTALLIN.
DR TIGRPFAMs; TIGR00928; purB; 1.
DR PROSITE; PS00163; FUMARATE_LYASES; 1.
DR Complete proteome; Lyase.
KW Complete proteome; Lyase.
SQ SEQUENCE 431 AA; 49603 MW; 493F79CBE814B9E5 CRC64;

Query Match 11.7%; Score 84; DB 2; Length 431;
Best Local Similarity 26.5%; Pred. No. 12;
Matches 26; Conservative 15; Mismatches 35; Indels 22; Gaps 2;

QY 33 GIFAIFSFYKLLQWYNRKSKKKRKEQIRIQEILGLLSYGAGVASPLLNVIHNPQS 92
DB 142 GVHAEPPTFGVKWALWYTEMQRNLQRFQVREIEVGKMSGAVG-----TFANIPPE 193

QY 93 VISATPIYKGPCTGVPSNRLQITSGTAENTRILNHD 130
DB 194 IESYVCKHLG-----IGTAPVSTQTLD 217

RESULT 6
QY 7A0G9 PRELIMINARY; PRT; 431 AA.
AC Q7A0G9;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Adenylosuccinate lyase.
GN Name=purB; OrderedLocusNames=MW1849;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RA "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL; AF004828; BAB95714.1; --
DR GO; GO:0016829; F:lyase activity; IEA.
DR InterPro; IPR003031; D:crystallin.
DR InterPro; IPR000362; Fumarate_lyase.
DR InterPro; IPR008948; L-Aspartase-like.

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RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; U41530; AAA83273.3; -.
DR PIR; T16774; T16774.
DR HSP; P56276; LFHG.
DR wormPep; SSSD1.1; CE29458.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS0853; FN3; 1.
DR PROSITE; PS0835; IG-LIKE; 3.
DR Hypothetical protein.
RW SEQUENCE 636 AA; 71728 MW; 2894A1E7428C0793 CRC64;

Query Match 11.5%; Score 82.5; DB 2; Length 636;
Best Local Similarity 23.7%; Pred. No. 27;
Matches 32; Conservative 19; Mismatches 43; Indels 41; Gaps 7;

QY 10 PPAPPNAPVEIVSSSTG---IIIVGIFAFIFSFYKLLQW---YNRKSKNKKRKEQ--- 61
Db 469 PPSFESNALRYGIADNVLPFIMLAAVFGLFCFACGLFAWRCHFNKKNKSKRKSNS 528

QY 62 --IRQIEIGLLSYGAGVASLPLNLVIAHPNPSVISATPIYKGPCTGVNSRLQITSGT 119
Db 529 TPSTKYQDYGRFTYGDSSS-----SQPG-----TETY-----EPSRLLD----- 565

QY 120 AEENTRLNHDGRNP 134
Db 566 -----DHEWRGP 572

RESULT 11
QY Q70696 PRELIMINARY; PRT; 734 AA.
AC Q70696;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE AGCF5939 (Fragment)
GN Name=agCG54493; ORFName=ENGANGG00000008214;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAA801008960; EAA11826.1; -.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007092; LRR_SDS22.
DR InterPro; IPR003591; LRR_cyp.
DR Pfam; PF00560; LRR; 10.
DR PRINTS; PRO0019; LEURICHRPT.
FT NON TER 1 734
FT NON TER 734 734
SQ SEQUENCE 734 AA; 80917 MW; A409AFD311EAB054 CRC64;

Query Match 11.4%; Score 82; DB 2; Length 734;
Best Local Similarity 26.9%; Pred. No. 35;
Matches 35; Conservative 15; Mismatches 36; Indels 44; Gaps 6;

QY 8 VOPPAPPNAPVEIVSSST-----GIIVGIFAFIFSFYKLLQWYNRKSKNKK 57
Db 620 VAPPPPPPPAAAVPVPSAAVPLAAPILPFGVPLALATVAPI-PILYE----- 665

QY 58 RKEQIREQIEIGLLSYGAGVASLPLNLVIAHPN-GSV-----ISATPIYKGPCTGVNSRL 112
Db 666 -----ASTSAPPPPPPVVVAHPHMGSGAGVSVVAASPTNGPLSSLPNT-- 710

QY 113 LQITSGTAAE 122
Db 711 IQKTHATDDE 720

RESULT 12
QY Q8CRT6 PRELIMINARY; PRT; 431 AA.
AC Q8CRT6;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Adenylosuccinate lyase.
GN OrderedLocusNames=SEI593;
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RX PubMed=12950922;
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
RT "Genome-based analysis of virulence genes in a non-biofilm-forming
RT Staphylococcus epidermidis strain (ATCC 12228).";
RL Mol. Microbiol. 49:1577-1593(2003).
DR EMBL; AB016749; AAO05192.1; -.
DR HSP; G9X010; IC3C.
DR GO; GO:0004018; F:adenylosuccinate lyase activity; IEA.
DR GO; GO:0016829; P:lyase activity; IEA.
DR GO; GO:0009152; P:purine ribonucleotide biosynthesis; IEA.
DR InterPro; IPR003031; D_crySTALLin.
DR InterPro; IPR000362; Fumarate_lyase.
DR InterPro; IPR008948; L-Aspartase-like.
DR Pfam; PF00206; Lyase 1; 1.
DR PRINTS; PRO0145; DCRYSTALLIN.
DR PRINTS; PRO0149; FUMARATELYASE.
DR TIGRFAMs; TIGR00928; purB; 1.
DR PROSITE; PS00163; FUMARATE_LYASES; 1.
KW Complete proteome; Lyase.
SQ SEQUENCE 431 AA; 49591 MW; 08D770CAB109B72A CRC64;

Query Match 11.2%; Score 80.5; DB 2; Length 431;
Best Local Similarity 34.0%; Pred. No. 27;
Matches 17; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

QY 33 GIFAFIFSFYKLLQWYNRKSKNKKRKEQIREQIEIGLLSYGAGV-ASLP 81
Db 142 GVHAEPTTFGVQNALWYTEMKNLRKPKVEKREIEVGKSGAVGTANIP 191

RESULT 13
QY Q6F2A9 PRELIMINARY; PRT; 443 AA.
AC Q6F2A9;
DT 01-OCT-2004 (TREMBlrel. 28, Created)
DT 01-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 01-OCT-2004 (TREMBlrel. 28, Last annotation update)
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Db      579 -ILSYSA--ASL-YTSLIYKN-----MTPVYTLTKGKATQISSPFLDDSSGDEEDSS 629
QY      123 --NTRILNHDGRNPDG 136
Db      630 RSSRLSESDARSRG 645

RESULT 15
Q8LP72
ID      Q8LP72      PRELIMINARY;      PRT;      633 AA.
AC      Q8LP72;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Receptor-like protein kinase.
OS      Nicotiana tabacum (Common tobacco).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC      lamiales; Solanales; Solanaceae; Nicotiana.
OX      NCBI_TaxID=4097;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=2191716; PubMed=11917080;
RA      Ito N., Takabatake R., Seo S., Hiraga S., Mitsuhashi I., Ohashi Y.;
RT      "Induced expression of a temperature-sensitive leucine-rich repeat
RT      receptor-like protein kinase gene by hypersensitive cell death and
RT      wounding in tobacco plant carrying the N resistance gene.";
RL      Plant Cell Physiol. 43:266-274(2002).
CC      -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR      EMBL; AB073628; BAC07504.2; -.
DR      GO; GO:0005524; F:ATP binding; IEA.
DR      GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      GO; GO:0006740; F:transferase activity; IEA.
DR      GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR      InterPro; IPR011009; Kinase_like.
DR      InterPro; IPR001611; LRR.
DR      InterPro; IPR007090; LRR plant.
DR      InterPro; IPR000719; Prot_kinase.
DR      InterPro; IPR008271; Ser_thr_pkin_AS.
DR      Pfam; PF00560; LRR; 6.
DR      Pfam; PF00069; Pkinase; 1.
DR      PRINTS; PR00019; LEURICHRPT.
DR      ProDom; PD000001; Prot_kinase; 1.
DR      PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW      ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW      Transferase.
SQ      SEQUENCE 633 AA; 70540 MW; 9221FF79372B4CD8 CRC64;

Query Match      11.0%; Score 79; DB 2; Length 633;
: Best Local Similarity 23.7%; Pred. No. 59;
Matches 40; Conservative 18; Mismatches 51; Indels 60; Gaps 6;

QY      11 PAPPNAPVEIV-----SSSTGIIITAVGIFAFIFSFYKLLQWYR 51
D5      255 PAPAPSHNVAPVHKRKKRKYRANPLGFGFAGSAISAV-----LLSVLFKLWNFFVR 309
QY      52 KSKNKKR----KEQIREQLGLSLYSYGAVSLPLNLVIAHNPVSGVISATPIYKGPCTGV 107
Db      310 KGKTDGSLTIYSPLIKKAEDLAFLEKEDGVASLEMG-----KGGCGEV 353
QY      108 -----PNSRLLOI-----TSGTAENTRILNHDGRNPDGSINV 140
Db      354 YRAELPGSNGKIIAIKKILQPPMDAAELAEEDTKALNKKQKRVKSEIQI 402

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Search completed: November 15, 2004, 14:57:34  
Job time : 198 secs